

# Recent Studies and Publications on Gut Microbiome and Health Effects (2017-February 2020)

## STUDIES

### 1. Microbiota-Immune Interaction In The Pathogenesis Of Gut-Derived Infection

Study shows that gut-derived infection is among the most common complications in patients who underwent severe **trauma, serious burn, major surgery, hemorrhagic shock or severe acute pancreatitis (SAP)** and it could cause **sepsis and multiple organ dysfunction syndromes (MODS)**, which are regarded as a leading cause of mortality in these cases. Researcher found that gut-derived infection is commonly caused by pathological translocation of intestinal bacteria or endotoxins, resulting from the dysfunction of the gut barrier. Limited information is available on the roles of intestinal microbial barrier in the development of gut-derived infection. They also found that advances of next-generation DNA sequencing techniques and its utilization has revolutionized the gut microecology, leading to novel views into the composition of the intestinal microbiota and its connections with multiple diseases.

*Source: Qirong Li, Research Institute of General Surgery, Jinling Hospital, Medical School, Nanjing University, Nanjing, China. Microbiota-Immune Interaction In The Pathogenesis Of Gut-Derived Infection. Front. Immunol., 07 August 2019. <https://doi.org/10.3389/fimmu.2019.01873>*

### 2. Echinacea Purpurea Protects Against Restraint Stress-Induced Immunosuppression In Balb/C Mice

New study shows that **Echishield** has protective effect against stress-induced changes in immunological function.

*Source: Park S, Department of Nutritional Science and Food Management, Ewha Womans University, Seoul, Korea. Echinacea purpurea protects against restraint stress-induced immunosuppression in Balb/C mice. Journal of Medicinal Food Vol. 21, No. 3. <https://doi.org/10.1089/jmf.2017.4073>.*

### 3. Short-Chain Fatty Acid Propionate Protects From Hypertensive Cardiovascular Damage

Study on mice shows that fatty acid propionate helps defend against the effects of high blood pressure, including atherosclerosis and heart tissue remodelling. Researchers found that beneficial gut microbes produce metabolites from natural dietary fibre, including a fatty acid called propionate. This substance protects against the harmful consequences of high blood pressure.

*Source: Dominik N. Müller, Experimental and Clinical Research Center, a Cooperation of Charité-Universitätsmedizin Berlin and Max Delbrück Center for Molecular Medicine, Germany. Short-chain fatty acid propionate protects from hypertensive cardiovascular damage. Circulation. 2019; 139:1407-1421. <https://doi.org/10.1161/CIRCULATIONAHA.118.036652>*

### 4. Dietary Restriction Improves Intestinal Cellular Fitness To Enhance Gut Barrier Function And Lifespan In D. Melanogaster

Study shows that flies on dietary restriction are protected from leaky gut and systemic inflammation as they age. Researchers found that dysbiosis is a contributor to leaky gut and ultimately the diet will be the primary driver in cellular changes leading to intestinal permeability.

*Source: Pankaj Kapahi, Buck Institute for Research on Aging, Novato, California, United States of America. Dietary restriction improves intestinal cellular fitness to enhance gut barrier function and lifespan in d. melanogaster. PLoS Genet 14(11): e1007777. <https://doi.org/10.1371/journal.pgen.1007777>*

### 5. Integrated In Vitro And In Silico Modeling Delineates The Molecular Effects Of A Synbiotic Regimen On Colorectal-Cancer-Derived Cells

Scientists found that a combination of prebiotics, such as dietary fibre, and probiotics, i.e. specific beneficial bacteria, reduces the expression of pro-carcinogenic and drug resistance genes. The combination leads to metabolic changes that affect the growth of cancer cells and may help treat diseases such as colorectal cancer (CRC).

*Source: Paul Wilmes, Luxembourg Centre for Systems Biomedicine, University of Luxembourg, Belvaux, Luxembourg. Integrated in vitro and in silico modeling delineates the molecular effects of a synbiotic regimen on colorectal-cancer-derived cells. Cel Rep, Volume 27, ISSUE 5, P1621-1632.e9, April 30, 2019. <https://doi.org/10.1016/j.celrep.2019.04.001>*

## 6. A Sparse Covarying Unit That Describes Healthy And Impaired Human Gut Microbiota Development

Study shows that a new type of therapeutic food designed specifically to repair the gut microbiome of malnourished children. They found that the therapeutic food is superior to standard therapy in clinical trial conducted at Bangladesh.

Study focuses on selectively boosting key growth-promoting gut microbes using ingredients present in affordable, culturally acceptable foods. The therapeutic food formulation contained a mixture of nutrients from chickpea, soy, bananas and peanuts.

*Source: Jeffrey I. Gordon, Edison Family Center for Genome Sciences and Systems Biology, and Center for Gut Microbiome and Nutrition Research, Washington University School of Medicine, St. Louis, USA. A sparse covarying unit that describes healthy and impaired human gut microbiota development. Science. 2019 Jul 12; 365(6449). pii: eaau4735.*

*DOI: 10.1126/science.aau4735 or <https://science.sciencemag.org/content/365/6449/eaau4732>*

## 7. 756-P: Changes In Gut Microbiota In Response To A Plant-Based Diet Are Related To Changes In Weight, Body Composition, And Insulin Sensitivity: A 16-Week Randomized Clinical Trial

Researcher found that after administrating plant-based diet till 16 weeks shows significantly reduction in the body weight among the vegan group (treatment effect average -5.8 kg), particularly due to a reduction in fat mass (average -3.9 kg) and in visceral fat. Insulin sensitivity also increased significantly in the vegan group.

*Source: Dr Hana Kahleova, Physicians Committee for Responsible Medicine (PCRM), Washington, DC, Padua, Italy. 756-P: Changes in gut microbiota in response to a plant-based diet are related to changes in weight, body composition, and insulin sensitivity: a 16-week randomized clinical trial. Diabetes 2019 Jun; 68(Supplement 1). <https://doi.org/10.2337/db19-756-P>*

## 8. Effects Of Dietary Fat On Gut Microbiota And Faecal Metabolites, And Their Relationship With Cardiometabolic Risk Factors: A 6-Month Randomized Controlled-Feeding Trial

New research found that when people boosted their fat intake to 40 percent of their daily diet for six months, the number of "good" gut bacteria decreased while "unhelpful" bacteria amounts increased. **Researcher found that they triggers inflammation in the body which leads to the development of metabolic disorders, such as diabetes and heart disease.**

*Source: Duo Li, Department of Food Science and Nutrition, Zhejiang University, Hangzhou, China. Effects of dietary fat on gut microbiota and faecal metabolites, and their relationship with cardiometabolic risk factors: a 6-month randomized controlled-feeding trial, Gut2019; 68: 1417-1429. <http://dx.doi.org/10.1136/gutjnl-2018-317609>*

## 9. US Immigration Westernizes The Human Gut Microbiome

Researchers found that immigrants begin losing their native microbes almost immediately after arriving in the U.S. and then acquire alien microbes that are more common in European-American people.

Study shows that communities migrating from Southeast Asia to the US developed some of the metabolic health issues, including obesity and diabetes, affecting immigrants to the country due to the changes in the microbiome.

*Source: Dan Knights, Bioinformatics and Computational Biology Program; Biotechnology Institute and Department of Computer Science and Engineering, University of Minnesota, Minneapolis, USA. 9. US immigration westernizes the human gut microbiome.*

*Cell. 2018 Nov 1; 175(4):962-972.e10. <https://doi.org/10.1016/j.cell.2018.10.029>*

## 10. Modulation Of The Gut Microbiota By Resistant Starch As A Treatment Of Chronic Kidney Diseases: Evidence Of Efficacy And Mechanistic Insights

A study has shown that resistant starch may alter gut microbial communities and confer changes in gut metabolites that lead to attenuated progression of chronic kidney disease.

*Source: Coughlan MT. Department of Diabetes, Central Clinical School, Monash University and Baker Heart Research Institute, Melbourne, Victoria, Australia. Modulation of the gut microbiota by resistant starch as a treatment of chronic kidney diseases: evidence of efficacy and mechanistic insights. Advances in Nutrition, Volume 10, Issue 2, March 2019, Pages 303-320, <https://doi.org/10.1093/advances/nmy068>*

## 11. Leveraging Human Microbiome Features To Diagnose And Stratify Children With Irritable Bowel Syndrome

To improve the treatment of children with irritable bowel syndrome (IBS), an investigator has developed a new battery of tests enables researchers to distinguish patients with IBS from healthy children and identifies correlations between certain microbes and metabolites with abdominal pain.

*Source: James Versalovic, Texas Children's Hospital and Baylor College of Medicine, Houston, Texas, USA. Leveraging human microbiome features to diagnose and stratify children with irritable bowel syndrome. J Mol Diagn. 2019 May; 21(3): 449-461. doi: [10.1016/j.jmoldx.2019.01.006](https://doi.org/10.1016/j.jmoldx.2019.01.006)*

## 12. High Primary Resistance To Metronidazole And Levofloxacin, And A Moderate Resistance To Clarithromycin In Helicobacter Pylori Isolated From Karnataka Patients

Researchers from India and Australia have found that a cancer-causing bacteria has become resistant to three commonly used antibiotics.

*Sources: Dr Eng Guan Chua, Marshall Centre for Infectious Diseases Research and Training, School of Biomedical Sciences, University of Western Australia, Crawley, WA, Australia. High primary resistance to metronidazole and levofloxacin, and a moderate resistance to clarithromycin in Helicobacter pylori isolated from Karnataka patients. Gut Pathog 11, 21 (2019). <https://doi.org/10.1186/s13099-019-0305-x>*

## 13. Gut Bacteria Selectively Promoted By Dietary Fibers Alleviate Type 2 Diabetes

Study shows that promotion of a selected group of gut bacteria by a diet high in diverse fibres lead to better blood glucose control, greater weight loss and better lipid levels in people with type 2 diabetes.

Researcher found that eating more of the right dietary fibres may rebalance the gut microbiota, or the ecosystem of bacteria in the gastrointestinal tract that help digest food and are important for overall human health.

*Source: Liping Zhao, State Key Laboratory of Microbial Metabolism and Ministry of Education Key Laboratory of Systems Biomedicine, School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, China and Department of Biochemistry and Microbiology and New Jersey Institute for Food, Nutrition, and Health, School of Environmental and Biological Sciences, Rutgers University, USA. Gut bacteria selectively promoted by dietary fibers alleviate type 2 diabetes. Science 09 Mar 2018: Vol. 359, Issue 6380, pp. 1151-1156. <https://doi.org/10.1126/science.aao5774>*

## 14. Salt-Responsive Gut Commensal Modulates TH17 Axis And Disease

Existing studies shows that a high intake of sodium increases chances of developing hypertension or high blood pressure. New research found that gut bacteria plays a crucial role in this context: probiotics will help to reverse the harmful effects of excessive salt.

*Source: Dominik N. Müller, Experimental and Clinical Research Center, a joint cooperation of Max-Delbrück Center for Molecular Medicine and Charité-Universitätsmedizin Berlin, Germany and DZHK (German Centre for Cardiovascular Research), partner site, Berlin, Germany. Salt-responsive gut commensal modulates TH17 axis and disease. Nature 551, 585-589 (2017). <https://doi.org/10.1038/nature24628>*

## 15. Community Structures And Genomic Features Of Undesirable White Colony-Forming Yeasts On Fermented Vegetables

Korean researchers have performed genome analysis on the white colony-forming yeast called film yeast or spoilage yeast in order to find out the yeast strains' and its potential metabolic effects in fermented foods. The researchers identified five representative yeast strains responsible for the white colony on the **kimchi** surface. One of the important results they found is that the strains did not have any known toxin-related genes.

*Source: Tae-Woon Kim, Microbiology and Functionality Research Group World Institute of Kimchi, Gwangju, Republic of Korea. Community structures and genomic features of undesirable white colony-forming yeasts on fermented vegetables. J Microbiol. (2019) 57: 30. <https://doi.org/10.1007/s12275-019-8487-y>*

## 16. Beyond Gut Feelings: How The Gut Microbiota Regulates Blood Pressure

In a Review, researchers describe the mechanisms by which the gut microbiota and its metabolites, including **short-chain fatty acids, trimethylamine N-oxide, and lipopolysaccharides**, act on downstream cellular targets to prevent or contribute to the pathogenesis of hypertension. These effects have a direct influence on tissues such as the kidney, the endothelium, and the heart. Finally, the role of the gut microbiota in resistant hypertension, the possible intergenerational effect of the gut microbiota on blood pressure regulation, and the promising therapeutic potential of gut microbiota modification to improve health and prevent disease are considered.

*Source: Marques FZ, Heart Failure Research Group, Baker Heart and Diabetes Institute and Australia and Department of Pharmacology, Faculty of Medicine, Nursing and Health Sciences, Monash University, Victoria, Australia. Beyond gut feelings: how the gut microbiota regulates blood pressure. Nat Rev Cardiol 15, 20-32 (2018). <https://doi.org/10.1038/nrcardio.2017.120>*

## 17. A Commensal Strain Of Staphylococcus Epidermidis Protects Against Skin Neoplasia

Scientists found that a strain of *Staphylococcus epidermidis* on healthy human skin exerts a selective ability to inhibit the growth of some cancers. This unique strain of skin bacteria produces a chemical that kills several types of cancer cells but does not appear to be toxic to normal cells.

*Source: Richard L. Gallo, Department of Dermatology, University of California, USA. Commensal strain of staphylococcus epidermidis protects against skin neoplasia. Science Advances 28 Feb 2018:Vol. 4, no. 2, eaao4502. <https://doi.org/10.1126/sciadv.aao4502>*

## 18. Impacts Of Microbiome Metabolites On Immune Regulation And Autoimmunity

New study shows that high salt consumption may prove fatal to certain gut bacteria which will contribute to high blood pressure and diseases affecting the immune system.

*Source: Ralf A. Linker, Department of Neurology, Friedrich-Alexander University, Erlangen, Germany. Impacts of microbiome metabolites on immune regulation and autoimmunity. Immunology. 2018 Jun; 154(2):230-238. <https://doi.org/10.1111/imm.12933>*

## 19. Broccoli Consumption Affects The Human Gastrointestinal Microbiota

Previous research studies show that consuming broccoli has health benefits in slowing down certain types of cancer. New study shows that microbial changes that occur in the human gut microbiome after eating broccoli are behind the vegetable's anti-cancer power.

*Source: Hannah Holscher, Division of Nutritional Sciences and Department of Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, United States. Broccoli consumption affects the human gastrointestinal microbiota. The Journal of Nutritional Biochemistry, Volume 63, January 2019, Pages 27-342019. <https://doi.org/10.1016/j.jnutbio.2018.09.015>*

## 20. Heart Failure Is Associated With Depletion Of Core Intestinal Microbiota

Data from German Centre for Cardiovascular Research (DZHK) has analysed the patients gut with heart failure and found that the important groups of bacteria are present less frequently and the gut flora is not as diverse as in healthy individuals. They also found that gut colonization is associated with the development and progress of heart failure.

*Source: Mark Luedde, Department of Internal Medicine III (Cardiology, Angiology and Intensive Care Medicine), University Medical Centre Schleswig-Holstein, Campus Kiel, Kiel, Germany. Heart failure is associated with depletion of core intestinal microbiota. ESC Heart failure, Volume4, Issue3, August 2017, Pages 282-290 2017. <https://doi.org/10.1002/ehf2.12155>*

## 21. Child Weight Gain Trajectories Linked To Oral Microbiota Composition

Study shows that weight gain trajectories in early childhood are related to the composition of oral bacteria (including beneficial bacteria) residing in the mouth of two-year-old children serve as an early indicator for childhood obesity.

*Source: Dr. Kateryna Makova, Center for Medical Genomics, Penn State University, University Park, PA, 16802, USA and Department of Biology, Penn State University, University Park, USA. Child weight gain trajectories linked to oral microbiota composition. Sci Rep 8, 14030 (2018). <https://doi.org/10.1038/s41598-018-31866-9>*

## 22. Loss Of Gut Barrier Integrity Triggers Activation Of Islet-Reactive T Cells And Autoimmune Diabetes

Researcher found that onset of autoimmunity in preclinical models of T1D is associated with alterations of the mucus layer structure and loss of gut barrier integrity. Study shows that breakage of the gut barrier integrity in BDC2.5XNOD mice carrying a transgenic T cell receptor (TCR) specific for a beta cell auto antigen leads to activation of islet-reactive T cells within the gut mucosa and onset of T1D. They also found that the intestinal activation of islet-reactive T cells requires the presence of gut microbiota and is abolished when mice are depleted of endogenous commensal microbiota by antibiotic treatment. Study results indicate that loss of gut barrier continuity can lead to activation of islet-specific T cells within the intestinal mucosa and to autoimmune diabetes and provide a strong rationale to design innovative therapeutic interventions in "at-risk" individuals aimed at restoring gut barrier integrity to prevent T1D occurrence.

*Source: Chiara Sorinia, Experimental Diabetes Unit, Division of Immunology, Transplantation and Infectious Diseases, IRCCS San Raffaele Scientific Institute, Italy and Immunology and Allergy Unit, Department of Medicine, Karolinska Institute, Stockholm, Sweden. Loss of gut barrier integrity triggers activation of islet-reactive T cells and autoimmune diabetes. PNAS July 23, 2019 116 (30) 15140-15149; first published June 10, 2019 <https://doi.org/10.1073/pnas.1814558116>*

## 23. The Ancestral And Industrialized Gut Microbiota And Implications For Human Health

Recent data shows that the microbiota of industrialized societies differs substantially from the recent ancestral microbiota of humans due to the rapid modernization, including medical practices and dietary changes which causing progressive deterioration of the microbiota which will contribute to various diseases prevalent in industrialized societies. **Researcher found that the ramifications of this incompatibility will be increased prevalence of NCCDs, which are driven by chronic, low levels of inflammation and/or a misregulated immune system.**

*Source: Erica D. Sonnenburg, Department of Microbiology and Immunology, Stanford University School of Medicine, Stanford, CA, USA. The ancestral and industrialized gut microbiota and implications for human health. Nat Rev Microbiol 17, 383-390 (2019). <https://doi.org/10.1038/s41579-019-0191-8>*

## 24. The Role Of The Microbiome In The Developmental Origins Of Health And Disease

Study shows that the variations in the composition and functional potential of the early-life microbiome are the result of lifestyle factors, such as mode of birth, breastfeeding, diet, and antibiotic usage. **Researcher found that variations in the composition of the early-life microbiome have been associated with specific disease outcomes, such as asthma, obesity, and neurodevelopmental disorders and this bacterial consortium act as a mediator between early lifestyle factors, health and disease.** They also found that variations in the microbial intrauterine environment may predispose neonates to specific health outcomes later in life. Study shows that the role of the microbiome in the Developmental Origins of Health and Disease and highlights the early-life critical window of susceptibility associated with microbiome development.

*Source: Stiemsma LT, Department of Epidemiology, Fielding School of Public Health, University of California, Los Angeles, Los Angeles, California. The Role Of The Microbiome In The Developmental Origins Of Health And Disease. Pediatrics April 2018, 141 (4) e20172437. <https://doi.org/10.1542/peds.2017-2437>*

## 25. The Microbiota Protects From Viral-Induced Neurologic Damage Through Microglia-Intrinsic TLR Signaling

Researchers found that gut microbes produce compounds which help prime immune cells to destroy harmful viruses in the brain and nervous system. Findings of the study shows that a healthy and diverse microbiota is essential for quickly clearing viruses in the nervous system to prevent paralysis and other risks associated with diseases such as multiple sclerosis.

*Source: June L Round, Department of Pathology, Division of Microbiology and Immunology, University of Utah School of Medicine, Salt Lake City, United States. The microbiota protects from viral-induced neurologic damage through microglia-intrinsic TLR signaling. eLife 2019;8:e47117. <https://doi.org/10.7554/eLife.47117.001>*



## 26. Intestinal Infection Triggers Parkinson's Disease-Like Symptoms In Pink1<sup>-/-</sup> Mice

Scientists found that mild gut infection results in development of symptoms related to motor and brain pathology resembling to Parkinson's disease (PD) in mice that carry a gene mutation known to be associated with the disorder in humans. Studies shows that an animal lacking the PINK1 gene, a gut infection causes overstimulation of the immune system which triggers an autoimmune reaction that kills dopaminergic neurons in the brain. They found that results will add weight to accumulating evidence implicating the gut-brain axis in PD.

*Source: Heidi M. McBride, Department of Microbiology and Immunology, McGill University, Montreal, Quebec, Canada. Intestinal infection triggers Parkinson's disease-like symptoms in Pink1<sup>-/-</sup> mice. Nature 571, 565-569 (2019). <https://doi.org/10.1038/s41586-019-1405-y>*

## 27. Gut Microbiota Modulation Accounts For The Neuroprotective Properties Of Anthocyanins

New Study data shows that HF (high fat) feeding strongly affected the composition of the gut microbiota and blackberry anthocyanin-rich extract (BE) will prevent some of the features of HF-diet induced dysbiosis (e.g. the increase of *Ruminococcus* and the decrease of *Oscillobacter*).

Researcher found that changes in gut bacterial genera induced by blackberry anthocyanin-rich extract (BE) are correlated with anti-neuro-inflammatory properties.

*Source: Conceição Calhau, Centre for Research in Health Technologies and Information Systems and Nutrition & Metabolism, NOVA Medical School, Portugal. Gut microbiota modulation accounts for the neuroprotective properties of anthocyanins. Sci Rep 8, 11341 (2018). <https://doi.org/10.1038/s41598-018-29744-5>*

## 28. Cutting Edge: Critical Roles For Microbiota-Mediated Regulation Of The Immune System In A Prenatal Immune Activation Model Of Autism

Researcher found that mother microbiome is a key contributor to the risk of autism and other neurodevelopmental disorders in her offspring.

Study shows that IL-17a molecule a key contributor to the development of autism-like symptoms in lab mice. They found that the microbiome will be modified easily, either through diet, probiotic supplements or fecal transplant and these approaches will restore a healthy equilibrium among the different microorganisms that live in the gut.

*Source: Dr John R Lukens, Center for Brain Immunology and Glia, Department of Neuroscience, School of Medicine and Graduate Program in Neuroscience, School of Medicine, University of Virginia, Charlottesville. Cutting edge: critical roles for microbiota-mediated regulation of the immune system in a prenatal immune activation model of autism. J Immunol August 1, 2018, 201 (3) 845-850; DOI: <https://doi.org/10.4049/jimmunol.1701755>*

## 29. Relationship Between The Gut Microbiome And Brain Function

It has become increasingly evident in recent years that the gut microbiome and the brain communicate in a bidirectional manner, with each possibly affecting the other's functions. Study shows that how the gut microbiome may affect brain function in adults, thereby having an impact on stress, anxiety, depression, and cognition. Many studies (in vitro, in vivo, and human) reporting an association between a change in the gut microbiome and functional changes in the brain. Researcher found that the mechanisms by which the brain affects the microbiome and the gastrointestinal tract to outline strategies for preventing or treating nervous system-related disturbances. They also found that supplemental probiotics to combat brain-related dysfunction offer a promising approach, provided future research elucidates their mode of action and possible side effects.

*Source: M Hasan Mohajeri, Department of Human Nutrition, DSM Nutritional Products, Basel, Switzerland. Relationship between the gut microbiome and brain function. Nutrition Reviews, Volume 76, Issue 7, July 2018, Pages 481-496, <https://doi.org/10.1093/nutrit/nuy009>*

### 30. The Microbiota-Gut-Brain Axis

Study shows that in the past 15 year the emergence of the microbiota (the trillions of microorganisms within and on our bodies) as one of the key regulators of gut-brain function which led to the appreciation of the importance of a distinct microbiota-gut-brain axis. Researchers found that the microbiota and the brain communicate with each other via various routes including the immune system, tryptophan metabolism, the vagus nerve and the enteric nervous system, involving microbial metabolites such as short-chain fatty acids, branched chain amino acids, and peptidoglycans. They also found that many factors can influence microbiota composition in early life, including infection, mode of birth delivery, use of antibiotic medications, the nature of nutritional provision, environmental stressors, and host genetics. Study reveals that at the other extreme of life, microbial diversity diminishes with aging and stress, in particular, significantly impact the microbiota-gut-brain axis at all stages of life.

*Source: John F. Cryan, APC Microbiome Ireland, Department of Anatomy and Neuroscience, Department of Psychiatry and Neurobehavioral Science, and Department of Physiology, University College Cork, Cork, Ireland. The microbiota-gut-brain axis. Physiological Reviews: Volume 99, Issue 4, October 2019, Pages 1877-2013. <https://doi.org/10.1152/physrev.00018.2018> and <https://www.physiology.org/doi/abs/10.1152/physrev.00018.2018>*

### 31. Mind And Gut: Associations Between Mood And Gastrointestinal Distress In Children Exposed To Adversity

Researcher found that children who face adversities such as parental separation are more likely to suffer from gastrointestinal symptoms which may lead to mental health issues in later life.

Study shows that gastrointestinal symptoms in children may have an impact on the brain and behavior as they grow to maturity. The findings indicate that gastrointestinal symptoms in young children will be a red flag to primary care physicians to detect future emotional health problems.

*Source: Bridget L. Callaghan, Department of Psychology, Columbia University, New York, USA and Department of Psychiatry, Melbourne University, Melbourne, Australia. Mind and gut: associations between mood and gastrointestinal distress in children exposed to adversity. Development And Psychopathology, Volume 32, Issue 1, February 2020, pp. 309-328. <https://doi.org/10.1017/S0954579419000087>*

### 32. The Neuroactive Potential Of The Human Gut Microbiota In Quality Of Life And Depression

Recent study shows a significant link between gut bacteria and mental health. Researchers studied the fecal microbiome data in conjunction with diagnoses of depression in 1,054 people taking part in the Flemish Gut Flora Project.

They found that two types of **bacteria from the genera *Coprococcus* and *Dialister*** were absent from the guts of people who are diagnosed with depression and who are on antidepressant medication. Researchers found that gut bacteria plays a role in causing depression. Study shows that many bacteria produce substances called neuroactive that will interact with the nervous system.

*Source: Jeroen Raes, Department of Microbiology and Immunology, Rega Institute for Medical Research, KU Leuven-University and VIB Center for Microbiology, Leuven, Belgium. The neuroactive potential of the human gut microbiota in quality of life and depression. Nat Microbiol 4, 623-632 (2019). <https://doi.org/10.1038/s41564-018-0337-x>*

### 33. Effects Of Regulating Intestinal Microbiota On Anxiety Symptoms: A Systematic Review

People who experience anxiety symptoms might be helped by taking steps to regulate the microorganisms in their gut using probiotic and non-probiotic food and supplements, suggests a review of 21 studies.

*Source: Jinghong Chen, Shanghai Key Laboratory of Psychotic Disorders, Shanghai Mental Health Centre, Shanghai Jiao Tong University School of Medicine, Shanghai, China. Effects of regulating intestinal microbiota on anxiety symptoms: a systematic review, General Psychiatry 2019; 32:e100056. <http://dx.doi.org/10.1136/psych-2019-100056>*

### 34. Gut Microbiota Modulate Neurobehavior Through Changes In Brain Insulin Sensitivity And Metabolism

Study shows that the gut bacteria play a key role in infusing negative feelings in the brains of obese people, causing depression and anxiety.

In mice researcher found that a high-fat diet has developed significantly more signs of anxiety, depression and obsessive behavior than animals on standard diets. They have also found that in mice with high-fat diets, two areas of the brain, the hypothalamus, which helps to control whole body metabolism, and the nucleus accumbens, important in mood and behavior, becomes insulin resistant.

*Source: C. Ronald Kahn, Section of Integrative Physiology and Metabolism, Joslin Diabetes Center and Department of Medicine, Harvard Medical School, Boston, USA. Gut microbiota modulate neurobehavior through changes in brain insulin sensitivity and metabolism. Mol Psychiatry 23, 2287-2301 (2018). <https://doi.org/10.1038/s41380-018-0086-5>*

### 35. Following Coffee Production From Cherries To Cup: Microbiological And Metabolomic Analysis Of Wet Processing Of Coffea Arabica

Scientists found that longer fermentation process lends a better taste to the coffee. Study shows that lactic acid bacteria play an important and positive role in processing coffee beans.

*Source: Luc De Vuyst, Research Group of Industrial Microbiology and Food Biotechnology, Faculty of Sciences and Bioengineering Sciences, Vrije Universiteit Brussel, Brussels, Belgium. Following coffee production from cherries to cup: microbiological and metabolomic analysis of wet processing of Coffea arabica. Appl Environ Microbiol 85:e02635-18. <https://doi.org/10.1128/AEM.02635-18>*

### 36. Association Between Usual Diet And Gut Microbiota Composition: Result From The Milieu Interieur Cross Sectional Study

A large-scale population-based study shows that the usual consumption of certain food items is associated with several gut microbial features, and extends the mechanistic arguments linking Western diet to an altered microbiota composition.

Researcher found that raw fruits and fish were positively associated with  $\alpha$ -diversity, whereas food items for which a limited consumption is generally recommended (fried products, sodas or sugary drinks, fatty sweet products, processed meats, ready-cooked meals, and desserts) were negatively associated with  $\alpha$ -diversity. They have also found that Fruits, fried products, ready-cooked meals, and cheese contributed to shifts within microbiota composition ( $\beta$ -diversity).

*Source: Valentin Partula, Sorbonne-Paris-Cité Research Center for Epidemiology and Statistics (CRESS), Nutritional Epidemiology Research Team (EREN) and University of Paris-VII Denis Diderot, Sorbonne-Paris-Cité University, Department of Life Sciences (SdV), Paris, France. Associations between usual diet and gut microbiota composition: results from the Milieu Intérieur cross-sectional study, The American Journal of Clinical Nutrition, Volume 109, Issue 5, May 2019, Pages 1472-1483, <https://doi.org/10.1093/ajcn/nqz029>*

### 37. Changes In The Gut Microbiota Of Urban Subjects During An Immersion In The Traditional Diet And Lifestyle Of A Rainforest Village

An international team of researchers has shown that immersing city dwellers in the traditional lifestyle and diet of a rainforest village for two weeks increases the diversity of the visiting children's but not the adults' gut microbiota. In a small pilot the team shows that the immersion visit did little to shift the adults' skin, oral, nasal and fecal microbiota.

*Source: Maria Gloria Dominguez-Bello, Department of Medicine, New York University Langone Medical Center, New York; Department of Biochemistry and Microbiology, Rutgers University, New Jersey; Department of Anthropology, New York University, New York, and Department of Anthropology, Rutgers University, New Jersey, USA. hanges in the gut microbiota of urban subjects during an immersion in the traditional diet and lifestyle of a rainforest village. mSphere 3:e00193-18. <https://doi.org/10.1128/mSphere.00193-18>*



### 38. Impact Of Edible Cricket Consumption On Gut Microbiota In Healthy Adults, A Double-Blind, Randomized Crossover Trial

A double-blind, randomized, crossover clinical trial has been conducted to evaluate the effects of consuming 25 g of whole cricket powder per day on human microbiome. Following the study, the researchers saw no signs of toxicity or intolerability for participants after eating crickets. No changes in lipid metabolism were observed, but there was a slight increase in alkaline phosphatase and a decrease in circulating pro-inflammatory cytokine TNF-alpha with cricket consumption. "These results are suggestive of an improvement in intestinal homeostasis," say researchers, "meaning that eating crickets may improve gut health and reduce systemic inflammation; however, more research is needed to understand these effects and underlying mechanisms.

Several changes in microbiota after eating cricket powder, including a prebiotic effect was also observed. Specifically, the researchers measured a significant increase in **Bifidobacterium animalis**, a probiotic known to inhibit pathogens, improve gastrointestinal function, and protect against diarrhea and foodborne pathogens.

*Source: Valerie J. Stull, Center for Sustainability and the Global Environment, University of Wisconsin-Madison, Madison, USA. Impact of edible cricket consumption on gut microbiota in healthy adults, a double-blind, randomized crossover trial. Sci Rep 8, 10762 (2018). <https://doi.org/10.1038/s41598-018-29032-2>*

### 39. Evidence Of Link Between Quorum Sensing And Sugar Metabolism In Escherichia Coli Revealed Via Cocystal Structures Of LsrK And HPr

New study shows that how the glucose generation from the food we eat affect bacterial signaling process called quorum sensing. Researcher found that during the process, individual bacteria secrete small signaling molecules called auto inducers and when the auto inducer signals build up they will reach a certain threshold where they are transported in tracellularly and the signals activate gene expression.

Studies like this will built scope for new antimicrobial therapies and even shape diet plans and exercise regimens to improve human health.

*Source: William E. Bentley, Institute for Bioscience and Biotechnology Research, University of Maryland and Fischell Department of Bioengineering, University of Maryland, College Park, USA. Evidence of link between quorum sensing and sugar metabolism in escherichia coli revealed via cocystal structures of LsrK And HPr. Science Advances 01 Jun 2018:Vol. 4, no. 6, eaar7063. <https://doi.org/10.1126/sciadv.aar7063>*

### 40. Longevity Extension In Drosophila Through Gut-Brain Communication

Scientists found that feeding fruit flies with a combination of probiotics and an herbal supplement called **Triphala** will promote flies longevity by 60 percent and protect them against chronic diseases associated with aging. The finding is explained by the "gut-brain axis," a bidirectional communication system between microorganisms residing in the gastrointestinal tract.

*Source: Satya Prakash, Biomedical and Cell Therapy Research Laboratory, Department of Biomedical Engineering, McGill University, Canada. Longevity extension in Drosophila through gut-brain communication. Sci Rep 8, 8362 (2018). <https://doi.org/10.1038/s41598-018-25382-z>*

### 41. A Human Gut Commensal Ferments Cranberry Carbohydrates To Produce Formate

Study shows that arterial metabolism of complex cranberry carbohydrates termed **xyloglucans** are not digested until reaching to the colon. This is significant as bifidobacteria interact with this dietary compound to potentially impact human host health through energy and metabolite production by bacterial utilization of these substrates.

Researcher found that cross-feeding occurs between bacteria in which one strain degrades the cranberry xyloglucan to make it available to a second strain. They found that the study will lead to novel foods or supplements which impact human health through rational manipulations of their microbiome.

*Source: David A. Sela, Department of Food Science, University of Massachusetts and Center for Microbiome Research, University of Massachusetts Medical School, Worcester, USA. A human gut commensal ferments cranberry carbohydrates to produce formate. Appl Environ Microbiol 83:e01097-17. <https://doi.org/10.1128/AEM.01097-17>*

## 42. The Intestinal Microbiota Programs Diurnal Rhythms In Host Metabolism Through Histone Deacetylase 3

In a new study researcher have found that the commensal, or good, bacteria that live in the guts of mammals, program the metabolic rhythms which govern the body's absorption of dietary fat.

Study shows that microbes program these so-called circadian rhythms by activating a protein named histone deacetylase 3 (HDAC3), which is made by cells that line the gut and these cells act as intermediaries between bacteria that aid in digestion of food and proteins and enable absorption of nutrients.

*Source: Lora V. Hooper, Department of Immunology, University of Texas Southwestern Medical Center and Howard Hughes Medical Institute, University of Texas Southwestern Medical Center, USA. The intestinal microbiota programs diurnal rhythms in host metabolism through histone deacetylase 3. Science 27 Sep 2019:Vol. 365, Issue 6460, pp. 1428-1434. <https://doi.org/10.1126/science.aaw3134>*

## 43. Cooking Shapes The Structure And Function Of The Gut Microbiome

Researcher found that in mice and humans cooking food fundamentally alters the microbiomes. Study shows that microbial changes attribute to the two key factors: cooked food allows the host to soak up more calories in the small intestine and leaving less for hungry microbes further down the gut; on the other hand, many raw foods contain potent antimicrobial compounds that appear to directly damage certain microbes.

*Source: Rachel N. Carmody, Department of Microbiology & Immunology, University of California San Francisco; Center for Systems Biology, Harvard University, Cambridge and Department of Human Evolutionary Biology, Harvard University, USA. Cooking shapes the structure and function of the gut microbiome. Nat Microbiol 4, 2052-2063 (2019). <https://doi.org/10.1038/s41564-019-0569-4>*

## 44. Prebiotic Supplementation Over A Cold Season And During Antibiotic Treatment Specifically Modulates The Gut Microbiota Composition Of 3-6 Year-Old Children

A study suggests that daily consumption of chicory root fiber in children aged 3–6 can keep the level of bifidobacteria higher and more stable, even during antibiotic treatment.

*Source: S. Theis , Beneo-Institute, Germany. Prebiotic supplementation over a cold season and during antibiotic treatment specifically modulates the gut microbiota composition of 3–6 year-old children. Beneficial Microbes: 10 (3)- Pages: 253 - 263(2019). <https://doi.org/10.3920/BM2018.0116>*

## 45. Food Contact Materials And Gut Health: Implications For Toxicity Assessment And Relevance Of High Molecular Weight Migrants

Studies shows that gut health is determined by an intact epithelial barrier and balanced gut microbiota, both involved in the regulation of immune responses in the gut and any disruption of this system contributes to the etiology of various non-communicable diseases, including intestinal, metabolic, and autoimmune disorders.

Researcher found that some food additives or food contaminants, such as pesticide residues and substances migrating from food contact materials (FCMs), may adversely affect the gut barrier or gut microbiota.

*Source: Ksenia J. Groh, Food Packaging Forum Foundation, Switzerland. Food contact materials and gut health: implications for toxicity assessment and relevance of high molecular weight migrants. Food and Chemical Toxicology, Volume 109, Part 1, November 2017, Pages 1-18. <https://doi.org/10.1016/j.fct.2017.08.023>*

## 46. The Small Intestine Converts Dietary Fructose Into Glucose And Organic Acids

Researchers found that in mice, fructose (sugar found in fruit) is processed mainly in the small intestine and not in the liver. Study shows that ability of the small intestine to process fructose is higher after a meal.

The researchers observed that excess fructose that is not absorbed by the small intestine continues through the intestine into the colon. As a consequence, it also comes into contact with the natural microbiotic flora of the large intestine and colon, known as the microbiome.

*Source: Joshua D Rabinowitz, Department of Chemistry and Lewis-Sigler Institute for Integrative Genomics, Princeton University, USA. 46.The small intestine converts dietary fructose into glucose and organic acids. Cell Metabolism, Volume 27, ISSUE 2, P351-361.e3, February 06,2018. <https://doi.org/10.1016/j.cmet.2017.12.016>*

#### 47. Dietary Fatty Acids Sustain Growth Of Human Gut Microbiota

Researcher found that the microbiome can quickly adapt from the bacterial equivalent of a typical western diet to one composed exclusively of dietary fats.

Study shows that adaptation will involve an increase in the populations of fatty-acid metabolizing species and a drop in those of protein and carbohydrate metabolizers. Scientist found that these changes will led to diminished production of short chain fatty acids and antioxidants, any alterations will negatively affect human health.

*Source: Oleg Paliy, Department of Biochemistry and Molecular Biology, Boonshoft School of Medicine, Wright State University, Dayton, USA. Dietary fatty acids sustain the growth of the human gut microbiota. Appl Environ Microbiol 84:e01525-18. <https://doi.org/10.1128/AEM.01525-18>*

#### 48. Bioremediation Of A Common Product Of Food Processing By A Human Gut Bacterium

Maillard reaction products (MRPs) formed during the food manufacturing process can have harmful health effects such as insulin resistance and obesity. A new study shows that human gut microbes can break down fructose lysine, a common MRP, into innocuous by-products.

These findings raise the prospect that it may be possible to use such knowledge of the gut microbiome to help develop healthier, more nutritious processed foods.

*Source: Jeffrey I. Gordon, Edison Family Center for Genome Sciences and Systems Biology, Washington University School of Medicine and Center for Gut Microbiome and Nutrition Research, Washington University School of Medicine, USA. Bioremediation of a common product of food processing by a human gut bacterium. Cell Host & Microbe, Volume 26, ISSUE 4, P463-477.e8, October 09, 2019. <https://doi.org/10.1016/j.chom.2019.09.001>*

#### 49. Role For Diet In Normal Gut Barrier Function: Developing Guidance Within The Framework Of Food-Labeling Regulations

Studies show that a reduction in intestinal barrier function play an important role in pathogenesis of many diseases, as it facilitates passage of injurious factors such as lipopolysaccharide, peptidoglycan, whole bacteria, and other toxins to traverse the barrier to damage the intestine or enter the portal circulation. Researchers found that in animal models and in vitro systems there are certain dietary interventions which can be used to reinforce the intestinal barrier to prevent the development of disease. Current review shows that diet can be used to fortify intestinal barrier function and such evidence would provide information on the development of healthier diets and serve to provide a framework by which federal agencies such as the US Food and Drug Administration can evaluate evidence linking diet with normal human structure/function claims focused on reducing risk of disease in the general public.

*Source: Gary D Wu, Division of Gastroenterology, Perelman School of Medicine, Univ. of Pennsylvania. Role for diet in normal gut barrier function: developing guidance within the framework of food-labeling regulations. Am J Physiol Gastrointest Liver Physiol, Volume 317, Issue 1, July 2019, Pages G17-G39 (2019). <https://doi.org/10.1152/ajpgi.00063.2019>*

#### 50. The Effects Of Vegetarian And Vegan Diets On Gut Microbiota

Study shows that a plant-based diet appears to be beneficial for human health by promoting the development of more diverse and stable microbial systems.

Researcher found that vegans and vegetarians have significantly higher counts of certain *Bacteroidetes*-related operational taxonomic units compared to omnivores, fibers (that is, non-digestible carbohydrates, found exclusively in plants) most consistently increase lactic acid bacteria, such as *Ruminococcus*, *E. rectale*, and *Roseburia*, and reduce *Clostridium* and *Enterococcus* species and polyphenols (abundant in plant foods) increase *Bifidobacterium* and *Lactobacillus*, which provide anti-pathogenic and anti-inflammatory effects and cardiovascular protection. They also found that high fiber intake also encourages the growth of species that ferment fiber into metabolites as short-chain fatty acids (SCFAs), including acetate, propionate, and butyrate.

Study indicate that the positive health effects of SCFAs are myriad, including improved immunity against pathogens, blood-brain barrier integrity, provision of energy substrates, and regulation of critical functions of the intestine and thus a vegetarian/vegan diet is effective in promoting a diverse ecosystem of beneficial bacteria to support both human gut microbiome and overall health.

*Source: Tomova A, Faculty of Medicine, Institute of Physiology, Comenius University in Bratislava, Slovakia. The effects of vegetarian and vegan diets on gut microbiota. Front Nutr. 2019; 6: 47 (2019). <https://doi.org/10.3389/fnut.2019.00047>*

## 51. Characterizing Microbiota-Independent Effects Of Oligosaccharides On Intestinal Epithelial Cells: Insight Into The Role Of Structure And Size : Structure-Activity Relationships Of Non-Digestible Oligosaccharides

Study shows that oligosaccharides have direct microbiota-independent effects on the intestinal barrier function and they also show the differences between individual galacto- and fructo-oligosaccharides. Researchers found that the microbiota-independent effect of oligosaccharides depends on the oligosaccharide structure, DP length and concentration.

*Source: Akbari P, Division of Veterinary Pharmacology, Pharmacotherapy and Toxicology, Institute for Risk Assessment Sciences and Division of Pharmacology, Utrecht Institute for Pharmaceutical Sciences Faculty of Science, Utrecht University, Netherlands. Characterizing microbiota-independent effects of oligosaccharides on intestinal epithelial cells: insight into the role of structure and size. Eur J Nutr 56, 1919-1930 (2017). <https://doi.org/10.1007/s00394-016-1234-9>*

## 52. Interspecies Competition Impacts Targeted Manipulation Of Human Gut Bacteria By Fiber-Derived Glycans

Humans choose food based on the way it looks, smells, and tastes. In the new study researcher found that the microbes in our guts use a different classification system. The classification system is based on the molecular components that make up different fibres. Investigators also found particular components of dietary fiber that encourage growth and metabolic action of beneficial microbes in the mouse gut.

*Source: Jeffrey Gordon, Edison Family Center for Genome Sciences and Systems Biology, Washington University School of Medicine and Center for Gut Microbiome and Nutrition Research, Washington University School of Medicine, USA. Interspecies competition impacts targeted manipulation of human gut bacteria by fiber-derived glycans. Cell, Volume 179, ISSUE 1, P59-73.e13, September 19, 2019. <https://doi.org/10.1016/j.cell.2019.08.011>*

## 53. Daily Sampling Reveals Personalized Diet-Microbiome Associations In Humans

Study shows that the interaction of bacteria in the gut with the food differs markedly between individuals. They found that the highly personalized nature of the gut microbiome requires dietary interventions to optimize the microbiome.

Researcher found that Foods with similar nutrition labels can have vastly different effects on the microbiome and Consequently, in order to promote or suppress a particular bacterial species through a food-based intervention, the diet may need to be individually tailored according to a person's specific microbiome.

*Source: Dan Knights, Biotechnology Institute, University of Minnesota, Saint Paul, MN 55108, USA and Department of Computer Science and Engineering, University of Minnesota, USA. Daily sampling reveals personalized diet-microbiome associations in humans. Cell Host and Microbe, Volume 25, ISSUE 6, P789-802.e5, June 12, 2019. <https://doi.org/10.1016/j.chom.2019.05.005>*

## 54. Effects of Fish n-3 PUFAs On Intestinal Microbiota And Immune System

Study shows that thousands of different microbial species are present in the human gut, and that there has been a significant variability of taxa in the microbiota composition among people.

Researcher found that several factors such as gestational age, mode of delivery, diet, sanitation and antibiotic treatment influence the bacterial community in the human gastrointestinal tract, and among these diet habits play a crucial role. They also found that the disturbances in the gut microbiota composition, i.e., gut dysbiosis, have been associated with diseases ranging from localized gastrointestinal disorders to neurologic, respiratory, metabolic, ocular, and cardiovascular illnesses. Experimental studies reveal that gut microbiota, n-3PUFAs, and host immune cells work together to ensure the intestinal wall integrity and this review indicate the current evidence concerning the links among gut microbiota, n-3 PUFAs intake, and human inflammatory disease.

*Source: Cinzia Parolini, Department of Pharmacological and Biomolecular Sciences, Università degli Studi di Milano, Italy. Effects of fish n-3 pufas on intestinal microbiota and immune system. Mar. Drugs 2019, 17(6), 374. <https://doi.org/10.3390/md17060374>*

## 55. Meta-Omics Analysis Of Elite Athletes Identifies A Performance-Enhancing Microbe That Functions Via Lactate Metabolism

New research has identified a type of bacteria found in the microbiomes of elite athletes that contributes to improved capacity for exercise. These bacteria, members of the genus *Veillonella*, are not found in the guts of sedentary people. Study shows that *Veillonella* metabolizes lactic acid which is produced by exercise and converts it into propionate (short chain fatty acid) which is utilized by human body to improve exercise capacity.

*Source: Aleksandar D. Kostic, Section on Pathophysiology and Molecular Pharmacology, Joslin Diabetes Center; Section on Islet Cell and Regenerative Biology, Joslin Diabetes Center and Department of Microbiology and Immunobiology, Harvard Medical School, Boston, USA. Meta-omics analysis of elite athletes identifies a performance-enhancing microbe that functions via lactate metabolism. Nat Med 25, 1104-1109 (2019). <https://doi.org/10.1038/s41591-019-0485-4>*

## 56. What Is The Microbiome?

Researchers found that microbiome composition is unlike the host genome as it is relatively constant; the microbiome is dynamic and it changes with early development, environmental factors such as diet and use of antibiotics and especially in response to disease. They also found that the most dramatic changes in composition will be occurred during infancy and early childhood.

Study on microbiome composition shows that the intestinal microbiome of an infant is affected by gestational age (full term or premature), mode of delivery (vaginal birth or caesarean section), type of feed (breast milk or formula feeds), maternal nutritional status (overweight or undernourished) and use of antibiotics. They also found that the complexity and plasticity of the infant microbiota during this early-life development is believed to be important in maintaining homeostasis with the host's immune system which has an impact on health later in life and by three years of age, the gut microbiota stabilizes similar to that of adults which is believed to be specific to individual quite like a fingerprint.

*Source: Amon P Sanderson, Centre for Immunobiology, Blizard Institute, London, UK. What is the microbiome? Archives of Disease in childhood-Education and Practice 2017; 102:257260. <http://dx.doi.org/10.1136/archdischild-2016-311643>*

## 57. The Role Of The Microbiome For Human Health: From Basic Science To Clinical Applications

Studies show that the gut microbiota changes dramatically during pregnancy and intrinsic factors (such as stress), in addition to extrinsic factors (such as diet, and drugs) influence the composition and activity of the gut microbiome throughout life.

Researcher found that microbial metabolites (e.g. short-chain fatty acids) affect gut-brain signaling and the immune response. Many studies highlighted that the gut microbiota has a regulatory role on anxiety, mood, cognition and pain which is exerted via the gut-brain axis. Data shows that ingestion of prebiotics or probiotics has been used to treat a range of conditions including constipation, allergic reactions and infections in infancy, and IBS. They also found that fecal microbiota transplantation (FMT) highly effective for treating recurrent *Clostridium difficile* infections. The gut microbiome affects virtually all aspects of human health, but the degree of scientific evidence, the models and technologies and the understanding of mechanisms of action vary considerably from one benefit area to the other. For a clinical practice to be broadly accepted, the mode of action, the therapeutic window, and potential side effects need to thoroughly be investigated.

*Source: Mohajeri MH, DSM Nutritional Products Ltd, Kaiseraugst, Switzerland. The role of the microbiome for human health: from basic science to clinical applications. Eur J Nutr 57, 1-14 (2018). <https://doi.org/10.1007/s00394-018-1703-4>*



## 58. Using Compositional Principal Component Analysis To Describe Children's Gut Microbiota In Relation To Diet And Body Composition

The use of compositional PCA has been investigated to describe the principal components (PCs) of gut microbiota in 5-year-old children and explore associations between microbiota components, diet, and BMI z-score.

Three gut microbiota PCs were found. PC1 (negative loadings on uncultured *Christensenellaceae* and *Ruminococcaceae*) was related to lower BMI z-scores and longer duration of breastfeeding (per month). PC2 (positive loadings on *Fusicatenibacter* and *Bifidobacterium*; negative loadings on *Bacteroides*) was associated with a lower intake of nuts, seeds, and legumes. When adjusted for fiber intake, PC2 was also associated with higher BMI z-scores. PC3 (positive loadings on *Faecalibacterium*, *Eubacterium*, and *Roseburia*) was associated with higher intakes of fiber and total non-starch polysaccharides. Study results suggest that specific gut microbiota components determined using compositional PCA are associated with diet and BMI z-score.

*Source: Rachael W Taylor, Department of Medicine, University of Otago, Dunedin, New Zealand. Using compositional principal component analysis to describe children's gut microbiota in relation to diet and body composition. The American Journal of Clinical Nutrition, Volume 111, Issue 1, January 2020, Pages 70-78, <https://doi.org/10.1093/ajcn/nqz270>*

## 59. Skin Exposure To Narrow Band Ultraviolet (UVB) Light Modulates The Human Intestinal Microbiome

This study shows that B ultraviolet light (UVB) is able to modulate the composition of the gut microbiome in humans, putatively through the synthesis of vitamin D. Vitamin D production was the main driver of the shift in the microbiome and skin UVB exposure and significantly increased gut microbial diversity. The largest effect was on increase in the relative abundance of *Lachnospiraceae bacteria* after the UVB light exposures. The study also revealed that both phototherapy and vitamin D supplementation influence the immune system and identified a novel skin-gut axis that may contribute to the protective role of UVB light exposure in chronic inflammatory diseases like multiple sclerosis (MS) and inflammatory bowel disease (IBD), but more research is warranted.

*Source: Bruce A. Vallance, Department of Pediatrics, BC Children's Hospital Research Institute, University of British Columbia, and BC Women's Hospital and Health Centre, Women's Health Research Institute, Vancouver, BC, Canada. Skin exposure to narrow band ultraviolet (uvb) light modulates the human intestinal microbiome. Front Microbiol. 2019; 10: 2410. <https://doi.org/10.3389/fmicb.2019.02410>*

## 60. Dietary Quality And The Colonic Mucosa-Associated Gut Microbiome In Humans

In an investigation on the associations between Healthy Eating Index (HEI)-2005 and the colonic mucosa-associated microbiota researchers found that the structure of the microbiota significantly differed by the scores for total HEI, total and whole fruits (HEI 1 and HEI 2), whole grains (HEI 6), milk products and soy beverages (HEI 7), and solid fat, alcohol, and added sugar (HEI 12). It was found that **a lower score for total HEI was associated with significantly reduced** relative abundance of *Parabacteroides*, *Roseburia*, and *Subdoligranulum* but higher *Fusobacterium*, **HEI 2 was associated with lower Roseburia but higher Bacteroides**, **HEI 7 was associated with lower Faecalibacterium and Fusobacterium but higher Bacteroides** and **HEI 12 was associated with lower Subdoligranulum but higher Escherichia and Fusobacterium**. Further, less abundant bacteria such as *Alistipes*, *Odoribacter*, *Bilophila*, and *Tyzzereella* were also associated with dietary quality. Hence, study result shows that a lower score for total HEI-2005 was significantly associated with reduced relative abundance of potentially beneficial bacteria but increased potentially harmful bacteria in the colonic mucosa of endoscopically normal individuals.

*Source: Li Jiao, Department of Medicine, Baylor College of Medicine (BCM); Dan L Duncan Comprehensive Cancer Center (BCM); Section of Gastroenterology, Michael E DeBakey Veterans Affairs Medical Center (MEDVAMC); Center for Innovations in Quality, Effectiveness, and Safety; Texas Medical Center Digestive Disease Center and Center for Translational Research on Translational Disease, Houston, USA. Dietary quality and the colonic mucosa-associated gut microbiome in humans. The American Journal of Clinical Nutrition, Volume 110, Issue 3, September 2019, Pages 701-712. <https://doi.org/10.1093/ajcn/nqz139>*

## 61. Red Wine Consumption Associated With Increased Gut Microbiota $\alpha$ -Diversity In 3 Independent Cohorts

This study shows that the gut of red wine drinkers contain a greater number of different bacterial species compared with those who did not drink it. White wine, beer, or spirits did not produce the same effect. It was found that moderate red wine consumption was associated with greater diversity and healthier gut microbiota as red wine are rich in beneficial polyphenols, which serve as “fuel” for the microbial population of the gut and also drinking red wine was associated with lower levels of obesity and “bad” cholesterol. Further, the effect of red wine on gut microbial diversity held true for three different study cohorts: one in the United States, another in the United Kingdom, and another in Belgium.

Source: Spector TD, Department of Twin Research Genetic Epidemiology, King's College London, London, UK. Red wine consumption associated with increased gut microbiota  $\alpha$ -diversity in 3 independent cohorts. *Gastroenterology*. 2020 Jan;158 (1):270-272.e2. <https://doi.org/10.1053/j.gastro.2019.08.024>

## 62. Dietary Prophage Inducers And Antimicrobials: Toward Landscaping The Human Gut Microbiome

This study shows that approximately 1011 viruses and microbial cells per gram of fecal matter (dry weight) in the large intestine are important to human health. The responses of three common gut bacteria species, and one opportunistic pathogen, to 117 commonly consumed foods, chemical additives, and plant extracts were tested. Researchers found that many compounds, including **Stevia rebaudiana** and **bee propolis extracts**, exhibited species-specific growth inhibition by prophage induction. It was also found that various foods may change the abundances of gut bacteria by modulating temperate phage. A novel path for landscaping the human gut microbiome has been suggested.

Source: Lance Boling, Department of Biology, San Diego State University, San Diego, CA, USA. Dietary prophage inducers and antimicrobials: toward landscaping the human gut microbiome. *Gut Microbes*, 2020. <https://doi.org/10.1080/19490976.2019.1701353>

## 63. Gut Commensal Derived-Valeric Acid Protects Against Radiation Injuries

A study on the effects of gut microbiota produced-valeric acid (VA) on radiation-induced injuries has found that VA exerted the most significant radioprotection among the short-chain fatty acids (SCFAs) and VA replenishment elevated the survival rate of irradiated mice, protected hematogenic organs, improved gastrointestinal (GI) tract function and intestinal epithelial integrity in irradiated mice. Further, high-throughput sequencing and Isobaric tags for relative and absolute quantitation

(iTRAQ) showed that oral gavage of VA restored the enteric bacteria taxonomic proportions, reprogrammed the small intestinal protein profile of mice following total abdominal irradiation (TAI) exposure and importantly, keratin 1 (KRT1) played a pivotal role in the radioprotection of VA. Study findings provide a new insight into gut microbiota-produced VA and that VA can be employed as a therapeutic option to mitigate radiation injury in pre-clinical settings.

Source: Ming Cui, Tianjin Key Laboratory of Radiation Medicine and Molecular Nuclear Medicine, Institute of Radiation Medicine, Chinese Academy of Medical Sciences and Peking Union Medical College, Tianjin, China. Gut commensal derived-valeric acid protects against radiation injuries. *Gut Microbes* 2020. <https://doi.org/10.1080/19490976.2019.1709387>

## 64. Continuous Pre- And Post-Transplant Exposure To A Disease-Associated Gut Microbiome Promotes Hyper-Acute Graft-Versus-Host Disease In Wild-Type Mice

This research investigates the individual contribution of the pre- and post-transplant gut microbiome to acute graft-versus-host disease (GVHD) using a well-studied mouse model.

It showed that priming wild-type mice via cohousing pre-transplant only is insufficient to accelerate GVHD, however, accelerated disease is observed in wild type (WT) mice cohoused post-transplant only and when mice are cohoused continuously, the effect of priming and exacerbation is additive, resulting in a greater acceleration of disease in WT mice beyond that seen with cohousing post-transplant only. It was also found that metagenomic analysis of the microbiome revealed pre-transplant cohousing is associated with the transfer of specific species within two as-yet-uncultured genera of the bacterial family **Muribaculaceae**; CAG-485 and CAG-873 whereas in post-transplant, it was observed that GVHD-associated blooms of **Enterobacteriaceae** members **Escherichia coli** and **Enterobacter hormaechei subsp. steigerwaltii**, and hyperacute GVHD gut microbiome distinct from that associated with delayed-onset disease (>10 days post-transplant). Study results shows that the importance of the peri-transplant microbiome in the susceptibility to acute GVHD post-transplant and also demonstrate the species-specific nature of this association.

Source: Kate L Bowerman, Australian Centre for Ecogenomics, School of Chemistry and Molecular Biosciences, The University of Queensland, Australia. Continuous pre- and post-transplant exposure to a disease-associated gut microbiome promotes hyper-acute graft-versus-host disease in wild-type mice. *Gut Microbes*, 2020. <https://doi.org/10.1080/19490976.2019.1705729>

## 65. Altered Gut Microbiome Composition In Patients With Vogt-Koyanagi-Harada Disease

This study was set up to identify abnormalities of gut microbiome composition in Vogt-Koyanagi-Harada (VKH) disease. Depleted butyrate-producing bacteria, lactate-producing bacteria and methanogens as well as enriched Gram-negative bacteria were identified in the active VKH patients, as well as in VKH patients of Mix enterotype and **Bacteroides enterotypes**. Changes of gut microbiome in the VKH patients were partially restored after an immunosuppressive treatment. It was also revealed that the disease susceptibility genotype HLA-DRA was associated with **Bacteroides sp.**, **Paraprevotella clara**, **Alistipes finegoldii** and **Eubacterium eligens**. A microbial marker profile including 40 disease-associated species was established to differentiate patients from controls. Study results also show that another microbial marker profile including 37 species is associated with the response to treatment and in an animal experiment it shows that transfer of gut microbiome from VKH patients could significantly exacerbate disease activity clinically and pathologically in the recipient mice. Finding of the study revealed that there is a distinct gut microbiome signature in VKH patients and they have an exacerbating effect of this gut microbiome on experimental autoimmune uveitis (EAU).

Source: Peizeng Yang, Chongqing Key Laboratory of Ophthalmology, Chongqing Eye Institute, The First Affiliated Hospital of Chongqing Medical University, Chongqing, China. Altered gut microbiome composition in patients with vogt-koyanagi-harada disease. Gut Microbes, 2020. <https://doi.org/10.1080/19490976.2019.1700754>

## 66. Effects Of Spaceflight On The Composition And Function Of The Human Gut Microbiota

This study shows that the composition and function of the gut microbiota are substantially affected by spaceflight; however, individual specificity is uncompromised. Further, resistance and virulence genes in the gut microbiota are affected by spaceflight, but the species attributions remain stable. Study findings indicate that spaceflight markedly affect the composition and function of the human gut microbiota, implying that the human gut microbiota is sensitive to spaceflight.

Source: Zizhong Liu, Key Lab of Space Nutrition and Food Engineering, China Astronaut Research and Training Centre, Beijing, China. Effects of spaceflight on the composition and function of the human gut microbiota. Gut Microbes, 2020. <https://doi.org/10.1080/19490976.2019.1710091>

## 67. Self-Assembling Cyclic d,l- $\alpha$ -Peptides As Modulators Of Plasma HDL Function Supramolecular Approach Toward Antiatherosclerotic Agents

A new supramolecular chemotype has been developed for altering HDL morphology and function which is guided by rational design and SAR-driven peptide sequence enumerations.

Researchers have synthesized and determined the HDL remodeling activities of over 80 cyclic d,l- $\alpha$ -peptides. A few distinct sequence motifs that are effective in vitro in remodeling human and mouse plasma HDLs to increase the concentration of lipid-poor pre-beta HDLs, which are key initial acceptors of cholesterol in the reverse cholesterol transport (RCT) process, and concomitantly promote cholesterol efflux from macrophage cells were identified and functional assays with various control peptides, such as scrambled sequences, linear and enantiomeric cyclic peptide variants, and backbone-modified structures that limit peptide self-assembly, provide strong support for the supramolecular mode of action. When the lead cyclic peptide c[wLwReQeR] was administered to mice (ip), it also promoted the formation of small, lipid-poor HDLs in vivo, displayed good plasma half-life ( $\approx$ 6 h), did not appear to have adverse side effects, and exerted potent anti-inflammatory effects in an acute in vivo inflammation assay.

The present study, involving a new structural class, represents a promising step toward new potential therapeutics to combat atherosclerosis.

Source: M. Reza Ghadiri, Department of Chemistry and The Skaggs Institute for Chemical Biology, The Scripps Research Institute and Cardiovascular Drug Discovery, Bristol-Myers Squibb Company, Pennington, US. ACS Cent. Sci. 2017, 3, 6, 639-646. <https://doi.org/10.1021/acscentsci.7b00154>

## 68. Walnuts And Vegetable Oils Containing Oleic Acid Differentially Affect The Gut Microbiota And Associations With Cardiovascular Risk Factors: Follow-Up Of A Randomized, Controlled, Feeding Trial In Adults At Risk For Cardiovascular Disease

An investigation into diet gut bacterial differences in individuals at increased cardiovascular risk following diets that replace SFAs with walnuts or vegetable oils has shown that the diet containing whole walnuts (WD) were most abundant in *Roseburia*, *Eubacterium eligens* group, *Lachnospiraceae* UCG001, *Lachnospiraceae* UCG004 and *Leuconostocaceae* in the standard western diet (SWD). They also found that a diet containing whole walnuts (WD) was also enriched in *Gordonibacter* relative to the walnut fatty acid-matched diet (WFMD) whereas *Roseburia* and *Eubacterium eligens* group were abundant following the walnut fatty acid-matched diet (WFMD), and *Clostridiales* vadin BB60 group and gut metagenome were most abundant following the oleic acid replaced ALA diet (ORAD) relative to the standard western diet (SWD). Study result indicates that *Lachnospiraceae* were inversely correlated with blood pressure and lipid/lipoprotein measurements following the diet containing whole walnuts (WD) and that the gut microbiota may contribute to the health benefits of walnut consumption in adults at cardiovascular risk.

Source: Penny M Kris-Etherton, Department of Nutritional Sciences, The Pennsylvania State University, University Park, USA. Walnuts and vegetable oils containing oleic acid differentially affect the gut microbiota and associations with cardiovascular risk factors: follow-up of a randomized, controlled, feeding trial in adults at risk for cardiovascular disease. *The Journal of Nutrition*, nxz289. <https://doi.org/10.1093/jn/nxz289>

## 69. Potential For Enriching Next-Generation Health-Promoting Gut Bacteria Through Prebiotics And Other Dietary Components

Study shows that the newly identified health-associated bacteria, such as *Faecalibacterium prausnitzii*, *Akkermansia muciniphila*, *Ruminococcus bromii* and *Roseburia species*, have emerged. Researcher found that the abundance of many of these bacteria is inversely correlated to several disease states while technological and regulatory hurdles may limit the use of strains from these taxa as probiotics and it should be possible to utilize prebiotics and other dietary components to selectively enhance their growth in situ. They also found that dietary components of potential relevance include well-established prebiotics, such as galacto-oligosaccharides, fructo-oligosaccharides and inulin, while other putative prebiotics, such as other oligosaccharides, polyphenols, resistant starch, algae and seaweed as well as host gut metabolites such as lactate and acetate, may also be applied with the aim of selectively and/or differentially affecting the beneficial bacterial community within the gastrointestinal environment. The present review provides an overview of the dietary components that could be applied in this manner.

Source: Paul D. Cotter, Teagasc Food Research Centre, Moorepark Fermoy, Ireland, APC Microbiome, Ireland. Potential for enriching next-generation health-promoting gut bacteria through prebiotics and other dietary components. *Gut Microbes*, 11:1, 1-20. <https://doi.org/10.1080/19490976.2019.1613124>

## 70. Human Fetal Lungs Harbor a Microbiome Signature

This study confirms the presence of a human fetal microbiome DNA signature in the early stage of pregnancy i.e. first trimester. Researchers found that there is a temporal change in fetal lung microbiome diversity during development which suggests maturational change with advancing gestational age. They also found the existence of a placental microbiome that bears some overlap with the corresponding human fetal lung microbiome based on overall microbiome analysis, as well as alpha and beta diversities. Materno-fetal microbial DNA transfer (and perhaps of other microbial products and whole live or dead bacteria) is a realistic possibility which may serve as a prime for the developing innate immune system of the fetus and help in establishment of a normal host-commensal relationship.

Source: Charitharth Vivek Lal, Women and Infant Centre University of Alabama, Pediatrics, Birmingham, Alabama, United States. Human fetal lungs harbor a microbiome signature. *Am J Respir Crit Care Med*. 2020 Jan 3. <https://doi.org/10.1164/rccm.201911-2127LE>



## 71. Restitution Of Gut Microbiota In Ugandan Children Administered With Probiotics (*Lactobacillus rhamnosus* GG And *Bifidobacterium animalis* subsp. *lactis* BB-12) During Treatment For Severe Acute Malnutrition

A study on gut microbiota (GM) evolution during rehabilitation from SAM and the impact of probiotics (*Lactobacillus rhamnosus* GG and *Bifidobacterium animalis* subsp. *lactis* BB-12) supplementation has revealed that the gut microbiota (GM) of children admitted to hospital with SAM showed distinct composition over admission (e.g. *Klebsiella* spp., and *Enterobacteriaceae* spp.), discharge (e.g. *Clostridiaceae* spp., *Veilonella dispar*) and follow-up (e.g. *Lactobacillus ruminis*, *Blautia* spp., *Faecalibacterium prausnitzii*), reaching similar  $\beta$ - and  $\alpha$ -diversity as healthy individuals. They also found that children with diarrhea had reduced distribution of *Bacteroidaceae*, *Lachnospiraceae*, increased *Enterobacteriaceae* and *Moraxellaceae*, and lower  $\alpha$ -diversity whereas children suffering from edematous SAM had diminished proportion of *Prevotellaceae*, *Lachnospiraceae*, *Ruminococcaceae* and a higher  $\alpha$ -diversity when compared to non-edematous SAM. Scientists observed that supplementation with probiotics did not influence  $\beta$ -diversity upon discharge or follow-up, but it increased the number of observed species whereas in children where the probiotic species were detected had lower cumulative incidence of diarrhea during the follow-up period. They also observed that probiotics treatment reduced the cumulative incidence of diarrhea during the outpatient phase, with the strongest effect in children where the administered probiotics could be detected in the GM. Study result shows that the GM of children with non-edematous and edematous SAM differ in composition, which have implications for future GM targeted treatments.

Source: Josue L Castro- Mejia, Department of Food Science, University of Copenhagen, Frederiksberg C, Denmark. Restitution of gut microbiota in Ugandan children administered with probiotics (*Lactobacillus rhamnosus* GG and *Bifidobacterium animalis* subsp. *lactis* BB-12) during treatment for severe acute malnutrition. *Gut Microbes*, 2020. <https://doi.org/10.1080/19490976.2020.1712982>

## 72. Antidepressant Treatment With Fluoxetine During Pregnancy And Lactation Modulates The Gut Microbiome And Metabolome In A Rat Model Relevant To Depression

Pregnancy and lactation segregate in terms of fecal microbiome diversity and composition, accompanied by changes in metabolite availability. This study shows that fluoxetine treatment alters important features of this transition from pregnancy to lactation most clearly in previously stressed dams, with lower fecal amino acid concentrations whereas amino acid concentrations, in turn, correlated negatively with the relative abundance of bacterial taxa such as *Prevotella* and *Bacteroides*. The relationship between antidepressant use during the perinatal period and maternal fecal metabolite availability in a rat model relevant to depression, possibly through parallel changes in the gut microbiome was also shown.

Source: Jocelien DA Olivier, Department of Neurobiology, Groningen institute of Evolutionary Life Sciences, University of Groningen, The Netherlands. Antidepressant treatment with fluoxetine during pregnancy and lactation modulates the gut microbiome and metabolome in a rat model relevant to depression. *Gut Microbes*, 2020. <https://doi.org/10.1080/19490976.2019.1705728>

## 73. Establishing High-Accuracy Biomarkers For Colorectal Cancer By Comparing Fecal Microbiomes In Patients With Healthy Families

Study shows that noninvasive gut microbiome (GM) biomarkers are promising for early CRC diagnosis as the GM varies significantly based on ethnicity, diet and living environment, suggesting varied GM biomarker performance in different regions.

Scientists performed metagenomic association analysis on stools from 52 patients and 55 corresponding healthy family members who lived together to identify gut microbiome (GM) biomarkers for colorectal cancer (CRC) in Chongqing, China. It was found that the GM of patients differed significantly from that of healthy controls. Findings of the study indicate that increased sensitivity and applicability of gut microbiome (GM) biomarkers compares with previous biomarkers significantly promoting the early diagnosis of CRC.

Source: Peiwu Yu, Department of General Surgery and Centre for Minimal Invasive Gastrointestinal Surgery, The first Hospital Affiliated to Army Medical University, Chongqing, China. Establishing high-accuracy biomarkers for colorectal cancer by comparing fecal microbiomes in patients with healthy families. *Gut Microbes*, 2020. <https://doi.org/10.1080/19490976.2020.1712986>



#### 74. Gut Feelings Begin in Childhood: the Gut Metagenome Correlates with Early Environment, Caregiving, and Behavior

Researchers conducted a metagenomic investigation among a cross-sectional sample of early school-aged children with a range of adverse experiences and caregiver stressors and relationships. The study shows that the taxonomic and functional composition of the gut microbiome correlates with behavior during a critical period of child development. They also found that both socioeconomic risk exposure and child behaviors associate with the relative abundances of specific taxa (e.g., *Bacteroides* and *Bifidobacterium species*) as well as functional modules encoded in their genomes (e.g., **monoamine metabolism**) that have been linked to cognition and health. Findings of the study suggest that caregivers may moderate the gut microbiome's link to environment and behaviors beyond the first few years of life.

*Source: Thomas J. Sharpton, Department of Microbiology, Oregon State University and Department of Statistics, Oregon State University, USA. Gut feelings begin in childhood: the gut metagenome correlates with early environment, caregiving, and behavior. mBio 11:e02780-19. <https://doi.org/10.1128/mBio.02780-19>*

#### 75. Environmental And Intrinsic Factors Shaping Gut Microbiota Composition And Diversity And Its Relation To Metabolic Health In Children And Early Adolescents: A Population-Based Study

Through characterization, by 16S sequencing, of the largest gut microbial population-based school-aged children cohort in Latin America (N = 926, aged 6–12 y) researchers found an associations of 14 clinical and environmental covariates, collectively explaining 15.7% of the inter-individual gut microbial variation. They also found that extrinsic factors such as markers of socioeconomic status have a major influence in the most abundant taxa and in the enterotypes distribution. Study result shows that age is positively correlated with higher diversity, but only in normal-weight children whereas this correlation was negative in overweight and obese children. Scientists also found that the co-abundance groups (CAGs) were associated with the presence of metabolic complications.

Findings of the study concluded that the presence of overweight and obesity could impair the microbial diversity maturation associated with age and it will be helpful to develop therapeutic approaches to improve metabolic status.

*Source: Samuel Canizales-Quinteros, Unidad De Genómica De Poblaciones Aplicada a La Salud, Facultad De Química and UNAM/Instituto Nacional De Medicina Genómica (INMEGEN), Mexico City, México. Environmental and intrinsic factors shaping gut microbiota composition and diversity and its relation to metabolic health in children and early adolescents: A population-based study. Gut Microbes, 2020. <https://doi.org/10.1080/19490976.2020.1712985>*

#### 76. Lactobacillus And Pediococcus Ameliorate Progression Of Non-Alcoholic Fatty Liver Disease Through Modulation Of The Gut Microbiome

This study shows that *L. bulgaricus*, *L. casei*, *L. helveticus*, and *P. pentosaceus KID7* supplementation can improve Non-Alcoholic Fatty Liver Disease (NAFLD) progression by modulating gut-microbiome and inflammatory pathway.

*Source: Ki Tae Suk, Institute for Liver and Digestive Diseases, Hallym University and Department of Internal Medicine, Hallym University College of Medicine, Republic of Korea. Lactobacillus and Pediococcus ameliorate progression of non-alcoholic fatty liver disease through modulation of the gut microbiome. Gut Microbes, 2020. <https://doi.org/10.1080/19490976.2020.1712984>*

#### 77. Validation Studies For Germ-Free Smad3<sup>-/-</sup> Mice As A Bio-Assay To Test The Causative Role Of Fecal Microbiomes In IBD

Scientists rederived Smad3<sup>-/-</sup> mice germ free (GF) to determine the potential of using these mice for testing the causative role of microbiomes in IBD. They found that fecal microbiomes from mice with IBD cause more severe gut inflammation in GF Smad3<sup>-/-</sup> and wild type mice compared to microbiomes from healthy mice and that **Helicobacter** induces gut inflammation within the context of other microbiomes but not by itself. They also found that germ free (GF) Smad3<sup>+/+</sup> and Smad3<sup>+/-</sup> mice given IBD microbiomes develop IBD despite their lack of disease in specific pathogen-free (SPF) conditions upon Helicobacter infection. Study results also show that both wild type C57BL/6 and 129 strains developed IBD upon fecal transfer whereas wild type Swiss Webster stock was not susceptible, indicating that the genetic background of recipient mice influences the severity of IBD following fecal transfer.

Finding of the study indicated that the microbiome is an independent risk factor contributing to IBD development, and careful characterization of new GF models is needed to understand potential sources of confounding factors influencing microbiome studies in these mice.

*Source: Jisun Paik, Department of Comparative Medicine, University of Washington, Seattle, USA. Validation studies for germ-free Smad3<sup>-/-</sup> mice as a bio-assay to test the causative role of fecal microbiomes in IBD. Gut Microbes, 11:1, 21-31,2019. <https://doi.org/10.1080/19490976.2019.1611151>*

## 78. Dietary Iron Variably Modulates Assembly Of The Intestinal Microbiota In Colitis-Resistant And Colitis-Susceptible Mice

Researchers investigated the impact of dietary iron on the intestinal microbiota, utilizing the conventionalization of germ-free mice as a model of a microbial community in compositional flux to recapitulate the instability of the IBD-associated intestinal microbiota.

Results showed that altering intestinal iron availability during community assembly modulated the microbiota in non-inflamed wild type (WT) and colitis-susceptible interleukin-10-deficient (Il10<sup>-/-</sup>) mice. It was also found that depletion of luminal iron availability promoted luminal compositional changes associated with dysbiotic states irrespective of host genotype, including an expansion of *Enterobacteriaceae such as Escherichia coli*. It was also found that mechanistic in vitro growth competitions confirmed that high-affinity iron acquisition systems in *E. coli* enhance its abundance over other bacteria in iron-restricted conditions, thereby enabling pathobiont iron scavenging during dietary iron restriction whereas distinct luminal community assembly was observed with dietary iron supplementation in WT versus Il10<sup>-/-</sup> mice, suggesting that the effects of increased iron on the microbiota differ with host inflammation status.

Study findings revealed that shifts in dietary iron intake during community assembly modulate the ecological structure of the intestinal microbiota and is dependent on host genotype and inflammation status.

*Source: R. Balfour Sartor, Department of Microbiology and Immunology, University of North Carolina; Department of Medicine, University of North Carolina and Centre for Gastrointestinal Biology and Disease, University of North Carolina, USA. Dietary iron variably modulates assembly of the intestinal microbiota in colitis-resistant and colitis-susceptible mice. Gut Microbes, 11:1, 32-50, 2019. <https://doi.org/10.1080/19490976.2019.1599794>*

## 79. In Search Of Stool Donors: A Multicenter Study Of Prior Knowledge, Perceptions, Motivators, And Deterrents Among Potential Donors For Fecal Microbiota Transplantation

This study identified the factors influencing willingness to donate stool. Researchers found that country of residence, age and occupation were not associated with willingness to donate stool and the factors increasing willingness to donate were: already a blood donor, male, altruism, economic benefit, knowledge of how FMT can help patients and positive attitudes towards FMT. They also found that factors decreasing willingness to donate were: stool collection unpleasant, screening process invasive, higher stool donation frequency, negative social perception of stool, and logistics of collection/transporting feces. Considering these variables could maximize donor recruitment and retention.

*Source: Dina Kao, Zeidler Ledcor Centre, Division of Gastroenterology, University of Alberta, Canada. In search of stool donors: a multicenter study of prior knowledge, perceptions, motivators, and deterrents among potential donors for fecal microbiota transplantation. Gut Microbes, 11:1, 51-62, 2019. <https://doi.org/10.1080/19490976.2019.1611153>*

## 80. The Association Between Gut Microbiome And Anthropometric Measurements In Bangladesh

Researchers investigated the relationship between the gut microbiota and anthropometric measurements among 248 participants from the Health Effects of Arsenic Longitudinal Study (HEALS) in Bangladesh.

It was found that higher BMI, mid-upper arm circumference, waist circumference, and waist-to-hip ratio were associated with a lower alpha diversity of fecal bacteria. They also found that relative abundance of the *genus Oscillospira* and the family S24-7 were inversely related to all measurements after correction for multiple testing whereas relative abundance of *genus Acidaminococcus and family Ruminococcaceae* were also associated with several measurements. Study showed positive associations of the *genus Acidaminococcus* with BMI, as well as waist and hip circumferences, and that these were stronger in women than in men.

*Source: Yu Chen, Department of Population Health and Environment Medicine, New York University School of Medicine, New York, USA. The association between gut microbiome and anthropometric measurements in Bangladesh, Gut Microbes, 11:1, 63-76, 2019. <https://doi.org/10.1080/19490976.2019.1614394>*

## 81. Serine-Rich Repeat Proteins From Gut Microbes

Serine-rich repeat proteins (SRRPs) from streptococci and staphylococci are O-glycosylated on serine or threonine residues and exported via an accessory secretion (aSec) system. This study found that in pathogens these adhesins contribute to disease pathogenesis and represent therapeutic targets. Further, the non-canonical aSec system in the genomes of gut microbes and characterization of their associated SRRPs is beginning to unfold, showing their role in mediating attachment and biofilm formation. Study results emphasise on the molecular and biochemical properties of SRRPs from gut symbionts, particularly *Lactobacilli*.

Source: Nathalie Juge, The Gut Microbes and Health Institute Strategic Programme, Quadram Institute Bioscience, Norwich Research Park, Norwich, UK, Gut Microbes, 2019. <https://doi.org/10.1080/19490976.2019.1602428>

## 82. Contribution Of Diet To Gut Microbiota And Related Host Cardiometabolic Health: Diet-Gut Interaction In Human Health

This study show that high-fat, low-carbohydrate diet is associated with unfavorable changes in gut microbiota, fecal microbial metabolites, and plasma proinflammatory factors in healthy young adults.

Source: Duo Li, Institution of Nutrition and Health, Qingdao University, China. Serine-rich repeat proteins from gut microbes, Gut Microbes, 11:1, 102-117, 2020. <https://doi.org/10.1080/19490976.2019.1697149>

## 83. Gut Microbiota Profiles In Critically Ill Patients, Potential Biomarkers And Risk Variables For Sepsis

The intestinal microbiota is involved in the health decline of such patients during ICU stays. This study aimed to assess the intestinal microbiota in critically ill patients with and without sepsis and to determine its impact on outcome variables, such as medical complications, ICU stay time, and mortality.

The study showed that the microbiota of ICU patients with sepsis has an increased abundance of microbes tightly associated with inflammation, such as *Parabacteroides*, *Fusobacterium* and *Bilophila species*. Further, female sex and aging would represent an increased risk for sepsis possibly because of some of their microbiota features and there is a remarkable loss of microbial diversity, during the ICU stay. Study results show that the abundance of pathogenic species, such as *Enterococcus spp.*, was differentially increased in sepsis patients who died, indicating these species as potential biomarkers for monitoring during ICU stay as these particular intestinal microbiota signatures could predict sepsis development in ICU patients.

Source: Gloria M. Agudelo-Ochoa, Food and Human Nutrition Research Group, Universidad de Antioquia (UdeA), Medellin, Colombia. Gut microbiota profiles in critically ill patients, potential biomarkers and risk variables for sepsis, Gut Microbes, 2020. <https://doi.org/10.1080/19490976.2019.1707610>

## 84. Temporal And Region-Specific Effects Of Sleep Fragmentation On Gut Microbiota And Intestinal Morphology In Sprague Dawley Rats

Previous Studies suggest that both sleep fragmentation (SF) and dysbiosis of the gut microbiome can lead to metabolic disorders, though the underlying mechanisms are largely unclear. Researchers investigated the effects of acute (6 days) and chronic (6 weeks) SF on rats by examining taxonomic profiles of microbiota in the distal ileum, cecum and proximal colon, as well as assessing structural and functional integrity of the gastrointestinal barrier and the impact of SF on a host function by evaluating inflammation and immune response.

Researchers found that in both acute and chronic SF induced microbial dysbiosis has significant perturbations in alpha- and beta-diversity whereas specific microbial populations were significantly altered throughout each of the three regions. They also found that chronic SF results from increased crypt depth in the distal ileum while there is an increase in the number of villi lining both the cecum and proximal colon. Study results show that there are additional changes with chronic SF which includes decreased microbial adhesion and penetration in the distal ileum and cecum, elevation in serum levels of the cytokine KC/GRO, and depressed levels of corticotropin. Findings of the study show that perturbations to microbial ecology and intestinal morphology intensify in response to prolonged SF and these changes are habitat specific.

Source: Victor Chan, Molecular Mechanisms Branch, Human Centered ISR Division, Airman Systems Directorate, Human Performance Wing, Air Force Research Laboratory, USA. Temporal and region-specific effects of sleep fragmentation on gut microbiota and intestinal morphology in Sprague Dawley rats. Gut Microbes, 2020. <https://doi.org/10.1080/19490976.2019.1701352>

## 85. Improvements In Metabolic Syndrome By Xanthohumol Derivatives Are Linked To Altered Gut Microbiota And Bile Acid Metabolism

Study shows that two hydrogenated xanthohumol (XN) derivatives,  $\alpha,\beta$ -dihydro-XN (DXN) and tetrahydro-XN (TXN), improved parameters of metabolic syndrome (MetS), a critical risk factor of cardiovascular disease (CVD) and type 2 diabetes, in a diet-induced obese murine model. Researchers found that administration of XN derivatives decreases intestinal microbiota diversity and abundance—specifically Bacteroidetes and Tenericutes—alters bile acid metabolism, and reduces inflammation. They also found that in WAT, TXN supplementation decreases pro-inflammatory gene expression by suppressing macrophage infiltration while transkingdom network analysis connects changes in the microbiota to bring improvements in MetS in the host. Findings of the study concluded that changes in the gut microbiota and bile acid metabolism bring improvements in obesity and MetS associated with administration of XN and its derivatives.

*Source: Zhang Y, Linus Pauling Institute, Oregon State University and School of Biological and Population Health Sciences, Oregon State University, USA. Improvements in Metabolic Syndrome by Xanthohumol Derivatives Are Linked to Altered Gut Microbiota and Bile Acid Metabolism. Mol Nutr Food Res. 2020 Jan; 64(1):e1900789. <https://doi.org/10.1002/mnfr.201900789>*

## 86. Intestinal Microbes Influence Development Of Thymic Lymphocytes In Early Life

Previous studies show that intestinal microbes influence the thymic homeostasis of PLZF-expressing cells in early life. In this study researchers found that impaired thymic development of PLZF+ innate lymphocytes in germ-free (GF) neonatal mice is restored by colonization with a human commensal, *Bacteroides fragilis*, but not with a polysaccharide A (PSA) deficient isogenic strain. They also found that plasmacytoid dendritic cells influenced by microbes migrate from the colon to the thymus in early life to regulate PLZF+ cell homeostasis whereas perturbations in thymic PLZF+ cells brought about by alterations in early gut microbiota persist into adulthood and are associated with increased susceptibility to experimental colitis. Findings of the study have identified a pathway of communication between intestinal microbes and thymic lymphocytes in the neonatal period that can modulate host susceptibility to immune-mediated diseases later in life.

*Source: Source: Nitya Jain, Mucosal Immunology and Biology Research Center, Massachusetts General Hospital for Children, Charlestown; Center for Computational and Integrative Biology, Massachusetts General Hospital and Department of Pediatrics, Harvard Medical School, Boston. Intestinal microbes influence development of thymic lymphocytes in early life. PNAS February 4, 2020 117 (5) 2570–2578. <https://doi.org/10.1073/pnas.1915047117>*

## 87. PTH Induces Bone Loss Via Microbial-Dependent Expansion Of Intestinal TNF+ T Cells And Th17 Cells

Previous studies have shown that parathyroid hormone (PTH) only causes bone loss in mice whose microbiota was enriched by the Th17 cell-inducing taxa segmented filamentous bacteria (SFB). In this study researcher found that SFB+ microbiota enabled PTH to expand intestinal TNF+ T and Th17 cells and increase their S1P-receptor-1 mediated egress from the intestine and recruitment to the bone marrow (BM) that causes bone loss whereas CXCR3-mediated TNF+ T cell homing to the BM upregulated the Th17 chemoattractant CCL20, which recruited Th17 cells to the BM. Findings of the study indicated that the mechanisms for microbiota-mediated gut–bone crosstalk in mice models of hyperparathyroidism may help to predict its clinical course and targeting the gut microbiota or T cell migration may represent therapeutic strategies for hyperparathyroidism.

*Source: Roberto Pacifici, Division of Endocrinology, Metabolism and Lipids, Department of Medicine, Emory Microbiome Research Center and Immunology and Molecular Pathogenesis Program, Emory University, Atlanta, USA. PTH induces bone loss via microbial-dependent expansion of intestinal TNF+ T cells and Th17 cells. Nat Commun 11, 468 (2020). <https://doi.org/10.1038/s41467-019-14148-4>*



## 88. Effect Of Cereal Soaking And Carbohydrase Supplementation On Growth, Nutrient Digestibility And Intestinal Microbiota In Liquid-Fed Grow-Finishing Pigs

This study shows that soaking the cereal fraction of a liquid diet prior to feeding (Csoak), and/or carbohydrase enzyme supplementation (ENZ) are likely to modulate both feed and intestinal microbial populations and improve feed efficiency (FE) in pigs.

Researcher found that an interaction between ENZ and Csoak for average daily gain (ADG) during the growing phase where pigs fed the Soak + ENZ diet had higher ADG than pigs fed the Fresh + ENZ diet whereas no treatment effect is found for ADG. They also found that enzyme supplementation increased total tract nutrient digestibility and reduced caecal VFA concentrations but did not improve pig growth or FE whereas both Csoak and ENZ modulated intestinal microbiota composition; increasing abundance of bacterial taxa that were negatively correlated with pig growth and reducing abundance of taxa positively correlated with pig growth and caecal butyrate concentration.

Scientist concluded from the study results that both strategies (Csoak and ENZ) improved nutrient digestibility in pigs and modulated intestinal microbiota composition.

*Source: Peadar G. Lawlor, Teagasc, Pig Development Department, Animal and Grassland Research and Innovation Centre, Ireland. Effect of cereal soaking and carbohydrase supplementation on growth, nutrient digestibility and intestinal microbiota in liquid-fed grow-finishing pigs. Sci Rep 10, 1023 (2020).*

<https://doi.org/10.1038/s41598-020-57668-6>

## 89. Inulin With Different Degrees Of Polymerization Protects Against Diet-Induced Endotoxemia And Inflammation In Association With Gut Microbiota Regulation In Mice

Investigation of the metabolic effects of inulin with different degrees of polymerization on high-fat diet-fed C57BL/6 J mice and evaluation of whether different health outcomes are related to regulation of the gut microbiota has shown that short-chain and long-chain inulins exert beneficial effects through alleviating endotoxemia and inflammation. Further, anti-inflammation is associated with a proportional increase in short-chain fatty acid-producing bacteria and an increase in the concentration of short-chain fatty acids whereas inulin might decrease endotoxemia by increasing the proportion of *Bifidobacterium* and *Lactobacillus*, and their inhibition of endotoxin secretion may also contribute to antiinflammation. The study shows that the beneficial health effects of long-chain inulin are more pronounced than those of short-chain inulin and that long-chain inulin is more dependent than short-chain inulin on species capable of processing complex polysaccharides, such as Bacteroides.

Scientist concluded that a good understanding of inulin-gut microbiota-host interactions helps to provide a dietary strategy that could target and prevent high-fat diet-induced endotoxemia and inflammation through a prebiotic effect.

*Source: Chang-Qing Ye; School of Public Health, Nantong University, China. Inulin with different degrees of polymerization protects against diet-induced endotoxemia and inflammation in association with gut microbiota regulation in mice. Sci Rep 10, 978 (2020). <https://doi.org/10.1038/s41598-020-58048-w>*

## 90. Growth Effects Of N-acylethanolamines On Gut Bacteria Reflect Altered Bacterial Abundances In Inflammatory Bowel Disease

Researchers found that N-acylethanolamines (NAEs), a class of endogenously produced signaling lipids are elevated in the stool of inflammatory bowel disease (IBD) patients and a T-cell transfer model of colitis, stimulated growth of species are over represented in IBD and inhibited that of species depleted in IBD in vitro. They also found that the effects of NAEs in complex microbial communities ex vivo, with *Proteobacteria* blooming and *Bacteroidetes* declines in the presence of NAEs. Finding of the study shows that NAEs as a class of metabolites are elevated in IBD and have the potential to shift gut microbiota towards an IBD-like composition.

*Source: Ramnik J. Xavier, Broad Institute of MIT and Harvard; Center for Microbiome Informatics and Therapeutics, Massachusetts Institute of Technology; Department of Molecular Biology and Centre for Computational and Integrative Biology, Massachusetts General Hospital, USA. Growth effects of N-acylethanolamines on gut bacteria reflect altered bacterial abundances in inflammatory bowel disease. Nat Microbiol (2020). <https://doi.org/10.1038/s41564-019-0655-7>*



## 91. Klebsiella Michiganensis Transmission Enhances Resistance To Enterobacteriaceae Gut Invasion By Nutrition Competition

This study addresses the functional consequences of the stochastic effects of microbiota perturbations, whereby microbial transmission through host interactions can facilitate reacquisition of beneficial commensals, minimizing the negative impact of antibiotics.

Researchers found that co-housed mice maintained colonization resistance after treatment with antibiotics, whereas most singly housed mice were susceptible to *E. coli*. Further, the ability to retain or share the commensal *Klebsiella michiganensis*, a member of the *Enterobacteriaceae family*, is sufficient for colonization resistance after treatment with antibiotics. Study results show that *K. michiganensis* generally out competed with *E. coli* in vitro, but in vivo administration of galactitol a nutrient that supports the growth of only *E. coli* to bi-colonized gnotobiotic mice abolished the colonization-resistance capacity of *K. michiganensis* against *E. coli*, supporting the idea that nutrient competition is the primary interaction mechanism while *K. michiganensis* hampered colonization of the pathogen *Salmonella*, prolonging host survival.

Source: Karina B. Xavier, Instituto Gulbenkian de Ciência, Portugal. *Klebsiella michiganensis* transmission enhances resistance to Enterobacteriaceae gut invasion by nutrition competition. *Nat Microbiol* (2020). <https://doi.org/10.1038/s41564-019-0658-4>

## 92. Characterizing The Microbiomes Of Antarctic Sponges: A Functional Metagenomic Approach

This study is an investigation into the community composition and metabolic potential of microbiomes from two abundant Antarctic sponges, *Leucetta antarctica* and *Myxilla species*. Genomic and taxonomic analyses show that both sponges harbor a distinct microbial community with high fungal abundance, which differs from the surrounding seawater whereas functional analyses reveal both sponge-associated microbial communities are enriched in functions related to the symbiotic lifestyle (e.g., CRISPR system, Eukaryotic-like proteins, and transposases), and in functions important for nutrient cycling. Researchers have found that both sponge microbiomes possess genes necessary to perform processes important in nitrogen cycling and carbon fixation. They also found that Antarctic sponge microorganisms prefer light-independent pathways for CO<sub>2</sub> fixation mediated by chemoautotrophic microorganisms. Hence study results show that how the unique metabolic potential of two Antarctic sponge microbiomes help these sponge holobionts survive in these inhospitable environments, and contribute to major nutrient cycles of these ecosystems.

Source: Nicole Trefault, GEMA Center for Genomics, Ecology & Environment, Facultad de Ciencias, Universidad Mayor, Santiago, Chile. *Characterizing the microbiomes of Antarctic sponges: a functional metagenomic approach*. *Sci Rep* 10, 645 (2020). <https://doi.org/10.1038/s41598-020-57464-2>

## 93. Microbiota-Targeted Maternal Antibodies Protect Neonates From Enteric Infection

This study shows that neonatal mice that lack the capacity to produce (Immunoglobulin G) IgG are protected from infection with the enteric pathogen enterotoxigenic *Escherichia coli* by maternal natural IgG antibodies against the maternal microbiota when antibodies are delivered either across the placenta or through breast milk.

It has been found that IgG derived from breast milk are crucial for protection against mucosal disease induced by enterotoxigenic *E. coli*. IgG also provides protection against systemic infection by *E. coli*. Pups used the neonatal Fc receptor to transfer IgG from milk into serum. The maternal commensal microbiota can induce antibodies that recognize antigens expressed by enterotoxigenic *E. coli* and other *Enterobacteriaceae species*. Induction of maternal antibodies against a commensal *Pantoea species* confers protection against enterotoxigenic *E. coli* in pups. Further, role of the microbiota in eliciting protective antibodies to a specific neonatal pathogen represents an important host defence mechanism against infection in neonates.

Source: Dennis L. Kasper, Department of Immunology, Harvard Medical School, Boston, USA. *Microbiota-targeted maternal antibodies protect neonates from enteric infection*. *Nature* 577, 543-548 (2020). <https://doi.org/10.1038/s41586-019-1898-4>

#### 94. Endogenous Murine Microbiota Member *Faecalibaculum Rodentium* And Its Human Homologue Protect From Intestinal Tumour Growth

Study demonstrates that changes in the microbiota and mucus composition are concomitant with tumorigenesis. They have identified two anti-tumourigenic strains of the microbiota ***Faecalibaculum rodentium*** and its human homologue, ***Holdemanella biformis*** that are strongly under-represented during tumorigenesis.

Scientists explored whether reconstitution of ApcMin/+ or azoxymethane and dextran sulfate sodium-treated mice with an isolate of ***F. rodentium*** (**F. PB1**) or its metabolic products reduced tumour growth. It was shown that both **F. PB1** and **H. biformis** produced short-chain fatty acids that contributed to control protein acetylation and tumour cell proliferation by inhibiting calcineurin and NFATc3 activation in mouse and human settings. Endogenous anti-tumourigenic bacterial strains were identified with strong diagnostic, therapeutic and translational potential.

*Source: Maria Rescigno, Humanitas Clinical and Research Center, IRCCS, Milan, Italy and Department of Biomedical Sciences, Humanitas University, Italy. Endogenous murine microbiota member Faecalibaculum rodentium and its human homologue protect from intestinal tumour growth. Nat Microbiol (2020). <https://doi.org/10.1038/s41564-019-0649-5>*

#### 95. Altered Microbiota, Fecal Lactate, And Fecal Bile Acids In Dogs With Gastrointestinal Disease

Researchers have found that there are significant increases in fecal lactate and decreases in secondary BA concentrations in dogs with CE (chronic enteropathy) and dogs with exocrine pancreatic insufficiency (EPI). Dogs with EPI hadve an increased abundance of ***Escherichia coli***, ***Lactobacillus***, and ***Bifidobacterium***; a decreased abundance of ***Fusobacterium*** and ***Clostridium hiranonis***; and a higher Dysbiosis Index when compared to healthy dogs. Further studies are necessary to determine the clinical utility of lactate and BA quantification in canine feces. These metabolites suggest functional alterations of intestinal dysbiosis and may become promising targets for further elucidating the role of the microbiota in health and disease.

*Source: Jan S. Suchodolski, Gastrointestinal Laboratory, Texas A&M University, Texas, United States of America. Altered microbiota, fecal lactate, and fecal bile acids in dogs with gastrointestinal disease. PLoS ONE 14(10): e0224454. <https://doi.org/10.1371/journal.pone.0224454>*

#### 96. Estradiol And High Fat Diet Associate With Changes In Gut Microbiota In Female ob/ob Mice

Scientists investigated whether estrogens and leptin modulate gut microbiota in **ovariectomized ob/ob (obese)** or **heterozygote (lean)** mice fed **high-fat diet (HFD)** that received either **17 $\beta$ -Estradiol (E2)** or vehicle implants. They found that E2 attenuated weight gain in both genotypes whereas both obesity (ob/ob mice) and E2 were associated with reduced gut microbial diversity. Study result shows that ob/ob mice exhibited lower species richness than control mice, while E2-treated mice had reduced evenness compared with vehicle mice. Further, E2 is associated with an increased abundance of the S24-7 family, while leptin is associated with increase in ***Coriobacteriaceae***, ***Clostridium*** and ***Lactobacillus***. Some taxa were affected by both E2 and leptin, suggesting these hormones alter gut microbiota of HFD-fed female mice. Understanding the role of E2 and leptin in regulating gut microbiota will provide important insights into hormone-dependent metabolic disorders in women.

*Source: Kalpana D. Acharya, Neuroscience Department, Wellesley College, USA. Estradiol and high fat diet associate with changes in gut microbiota in female ob/ob mice. Sci Rep 9, 20192 (2019). <https://doi.org/10.1038/s41598-019-56723-1>*

#### 97. Dietary Restriction Increases Protective Gut Bacteria To Rescue Lethal Methotrexate-Induced Intestinal Toxicity

Researchers have found that DR significantly reduces intestinal inflammation, preserves the number of basal crypt PCNA-positive cells, and protects the function of **intestinal stem cells (ISCs)** after MTX treatment. Furthermore, ablating intestinal microbiota by broad-spectrum antibiotics completely eliminates the protective effect achieved by DR. 16S rRNA gene deep-sequencing analysis and that short-term DR significantly increases the ***Lactobacillus*** genus, with ***Lactobacillus rhamnosus GG*** **gavage** partially mimicking the rescue effect of DR on the intestines of ad libitum fed mice exposed to lethal-dose MTX. The current study reveals that DR could be a highly effective way to alleviate the lethal injury in the intestine after high-dose MTX treatment, which is functionally mediated by increasing the protective intestinal microbiota taxa in mice.

*Source: Si Tao, Jiangxi Key Laboratory of Clinical and Translational Cancer Research and Department of Oncology, the Second Affiliated Hospital of Nanchang University, China. Dietary restriction increases protective gut bacteria to rescue lethal methotrexate-induced intestinal toxicity. Gut Microbes, 2020. <https://doi.org/10.1080/19490976.2020.1714401>*

## 98. Effect Of Mycobiome Diet On Gut Fungal And Bacterial Communities Of Healthy Adults

This study was conducted to evaluate the effectiveness of the mycobiome diet on the human gut microbiome in general and the gut mycobiome.

Researchers have found that the mycobiome diets are highly successful at reducing pathogenic ***Candida species*** and within two weeks, *Candida* species overall decreases by 72.4%; ***C. albicans*** in particular decreases 1.42-fold, while ***C. tropicalis*** remain undetected after 4 weeks. There levels of beneficial bacteria significantly increase, specifically ***Faecalibacterium prausnitzii***, ***Bifidobacterium***, ***Roseburia***, ***Lactobacillus***, and ***Bacteroides***. Furthermore, pathogenic bacteria decrease significantly, including ***Escherichia coli***, ***Bacteroides fragilis***, and ***Clostridium***. The changes in the microbiome structure are accompanied with improvement in digestive symptoms, weight loss, less fatigue, more energy, better sleep, and fewer cravings for empty-calorie foods.

According to study result adhering to the mycobiome diet for 4 weeks led to positive shifts in fungal and bacterial microbiome communities concurrently with positive improvement in GI symptoms and overall health.

*Source: Ghannoum M, Case Western Reserve University and University Hospitals Cleveland Medical Center, USA. Effect of Mycobiome diet on Gut Fungal and Bacterial Communities of Healthy Adults. J Prob Health. 7:215. DOI: 10.35248/2329-8901.19.7.215*

## 99. The i-screen: A Versatile Preclinical Platform For Gut Microbiota Studies

Scientist has developed a method, called i-screen, to evaluate the effects of compounds on the human gut microbiota. This i-screen is an in vitro system that allows the anaerobic cultivation of microorganisms obtained from fecal material, and therefore, representative of the highly diverse colonic microbiota. By means of specific analyses, the effects of test compounds on the gut microbiota composition and metabolic activity can be assessed. The i-screen has proven to be an effective and versatile experimental model of the gut microbiota, routinely applied to evaluate the effects of food ingredients and drugs. This system constitutes a valid contribution to product development and a starting point for a better understanding of the role of gut microbiota in host health.

*Source: Frank Schuren, Microbiology and Systems Biology Group, Netherlands Organization for Applied Scientific Research, Netherlands. The i-screen: A Versatile Preclinical Platform for Gut Microbiota Studies. J Prob Health. 7:212. DOI: 10.35248.2329-8901.19.7.212*

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